

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									2CBA 4	
1568	1cvm	A	167	680	0	0.06	-0.11		PROSTAGLANDIN H2 SYNTHASE-2; CHAIN: A, B; 9-MER; CHAIN: F;	OXIDOREDUCTASE COX-2, CYCLOOXYGENASE, PROSTAGLANDIN, ARACHIDONATE 2 ENDOPEROXIDE
1568	1d2v	A	139	241	3.4e-41	-0.76	0.19		MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	OXIDOREDUCTASE HEME-PROTEIN, PEROXIDASE, OXIDOREDUCTASE, PEROXIDASE-2 BROMIDE COMPLEX
1568	1d2v	C	232	714	0	0.61	1.00		MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	OXIDOREDUCTASE HEME-PROTEIN, PEROXIDASE, OXIDOREDUCTASE, PEROXIDASE-2 BROMIDE COMPLEX
1568	1d1y	A	167	580	0	0.22	1.00		PROSTAGLANDIN H2 SYNTHASE-1; CHAIN: A;	OXIDOREDUCTASE ARACHIDONIC ACID MEMBRANE PROTEIN, PEROXIDASE, DIOXYGENASE
1569	1gjc	A	51	82	0.0045	-0.65	0.00		ADRENODOXIN REDUCTASE; CHAIN: A;	OXIDOREDUCTASE ADR, NADPH: ADRENODOXIN OXIDOREDUCTASE; FLAVOENZYME, MAD ANALYSIS, ELECTRON TRANSFERASE
1569	1e15	A	62	430	6.8e-37	0.31	0.81		SARCOSINE OXIDASE; CHAIN: A, B;	OXIDOREDUCTASE
1569	1f1m	A	61	437	8.5e-53	-0.04	0.03		FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A, M; FUMARATE REDUCTASE IRON-SULFUR PROTEIN; CHAIN: B, N; FUMARATE REDUCTASE 15 KD HYDROPHOBIC PROTEIN; CHAIN: C, O; FUMARATE REDUCTASE 13 KD	FLAVOPROTEIN, OXIDASE COMPLEX II, COMPLEX II; COMPLEX II; FUMARATE REDUCTASE; COMPLEX II, SUCCINATE DEHYDROGENASE, 2 RESPIRATION, OXIDOREDUCTASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1569	1lpf	A	46	82	0.003	-0.23	0.07		HYDROPHOBIC PROTEIN; CHAIN: D, P;	
									OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) COMPLEX WITH ILPF 3 FLAVIN-ADENINE- DINUCLEOTIDE (FAD) ILPF 4	
1569	1qla	A	61	437	1.2e-43	-0.34	0.04		FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A, D; FUMARATE REDUCTASE IRON-SULFUR PROTEIN; CHAIN: B, E; FUMARATE REDUCTASE CYTOCHROME B SUBUNIT; CHAIN: C, F;	OXIDOREDUCTASE FUMARATE REDUCTASE, SUCGINATE DEHYDROGENASE, RESPIRATORY 2 CHAIN, CITRIC ACID CYCLE, FLAVOPROTEIN, IRON-SULFUR PROTEIN, DIHAEM CYTOCHROME B
1569	1qp8	A	28	434	8.5e-29	0.04	-0.09		FLAVOCYTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A, D;	OXIDOREDUCTASE OXIDOREDUCTASE
1569	3lad	A	46	83	0.0015	-0.09	0.09		OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	
1571	1tona		125	230	5.1e-24	0.60	0.83		T-FIMBRIN; CHAIN: NULL;	ACTIN-BINDING PROTEIN ACTIN- BINDING, PHOSPHORYLATION
1571	1aon		127	230	1.5e-29	0.54	0.40		T-FIMBRIN; CHAIN: NULL;	ACTIN-BINDING PROTEIN ACTIN- BINDING, PHOSPHORYLATION
1571	1bhd	A	123	232	4.5e-35			74.32	UTROPHIN; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOG, ACTIN BINDING, STRUCTURAL PROTEIN
1571	1bhd	A	126	232	1.7e-34	0.84	1.00		UTROPHIN; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1571	1bhd	A	127	232	4.5e-35	0.85	1.00		UTROPHIN; CHAIN: A, B;	HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN
1571	1bhr	A	126	235	8.5e-43			86.88	SPECTRIN BETA CHAIN; CHAIN: A;	HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN
1571	1bkr	A	127	235	8.5e-43	0.86	1.00		SPECTRIN BETA CHAIN; CHAIN: A;	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
1571	1dxx	A	126	233	1e-35	0.69	1.00		DYSTROPHIN; CHAIN: A, B, C, D;	ACTIN-BINDING CALPONIN HOMOLOGY (CE) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
1571	1qag	A	126	233	5.1e-35	0.68	1.00		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN-BINDING, UTROPHIN
1574	1e4z	A	202	562	0	0.24	1.00		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
1574	1e4z	A	212	564	0			131.07	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
1575	1epf	A	115	207	1e-06	0.66	0.05		NEURAL CELL ADHESION	CELL ADHESION NCAM; NCAM,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1575	1ev2	E	113	188	3e-05	-0.30	0.13		MOLECULE; CHAIN: A, B, C, D;	IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
									FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGF2; FGF2; IMMUNOGLOBULIN FOLD-LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IGH-LIKE DOMAINS, B-TREFOIL FOLD
1575	1hng	A	115	212	1.5e-06	0.13	0.04		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3	
1575	1dt		113	186	1.2e-05	-0.25	0.00		TITIN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27, TITIN I27 REPEAT 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN
1575	2fcb	A	105	206	7.5e-06	0.13	0.01		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1576	1d0s	A	484	664	9e-10	0.08	-0.19		NICOTINATE MONONUCLEOTIDE:5,6-CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF; PHOSPHORIBOSYL TRANSFERASE
1576	1d0s	A	491	643	7.5e-10	0.14	-0.20		NICOTINATE MONONUCLEOTIDE:5,6-CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF; PHOSPHORIBOSYL TRANSFERASE
1576	1e0t		138	324	1.5e-10	0.05	-0.20		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1576	1e0t		266	476	6e-10	0.03	-0.19		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1578	1bp3	B	102	212	6e-11	0.02	-0.14		GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR
1578	1bp3	B	31	224	6e-11			53.09	GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR;	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR,



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1578	1bpv		119	218	9e-10	-0.00	-0.08		CHAIN: B; TITIN; CHAIN: NULL;	HORMONE/GROWTH FACTOR CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1578	1o8p	A	124	211	3e-08	0.08	-0.09		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
1578	1elb		41	199	6e-10	0.09	0.04		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICTB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICTB 4 (RESIDUES 610 - 814) ICTB 5	
1578	1l6f	B	124	211	3e-10	0.23	-0.14		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE- RECEPTOR COMPLEX
1578	1f6h	A	35	315	7.5e-06			56.61	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1578	1mfh		34	224	1.2e-09			57.30	FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1578	1mfh		37	199	1.2e-09	0.30	0.34		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1578	1q4	A	35	211	4.5e-07			55.27	TENASCIN; CHAIN: A, B;	GLYCOPROTEIN STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE II, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1578	1uf		124	199	1.5e-09	-0.03	0.59		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	
1578	2fbb	A	124	213	9e-10	0.11	0.10		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPE III DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1579	1b6b	B	511	627	8.5e-14	0.42	0.80		ARYLALKYLAMINE N- ACETYLTRANSFERASE, CHAIN: A, B;	TRANSFERASE ACETYLTRANSFERASE
1579	1b04	A	523	622	1.7e-10	-0.56	0.10		SERRATIA MARCESCENS AMINOGLYCOSIDE-3-N- CHAIN: A, B;	TRANSFERASE AMINOGLYCOSIDE 3-N-ACETYLTRANSFERASE, EUBACTERIAL 2 AMINOGLYCOSIDE RESISTANCE, GCN5-RELATED N- ACETYLTRANSFERASE, 3 COA- BINDING
1579	1gww	A	511	627	5.1e-13	0.50	0.86		SEROTONIN N- ACETYLTRANSFERASE; CHAIN: A;	TRANSFERASE N-ACETYL TRANSFERASE
1579	1qam	A	487	624	5.1e-12	-0.15	0.04		HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE
1579	1qam	A	537	653	1.5e-14	0.08	0.00		HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T A A	END A A	Psi Blast	Verify score	FMF score	SEQFOL D score	Compound	PDB annotation
1580	1b6b	B	616	732	3.4e-19	0.43	0.83		ARYLALKYLAMINE N-ACETYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE ACETYLTRANSFERASE
1580	1b87	A	626	749	1.7e-11	-0.18	0.16		AMINOGLYCOSIDE N6-ACETYLTRANSFERASE TYPE I; CHAIN: A;	TRANSFERASE AAC; AMINOGLYCOSIDE 6-N-ACETYLTRANSFERASE, ANTIBIOTIC 2 RESISTANCE, ACETYL COENZYME A
1580	1b04	A	627	727	5.1e-12	-0.18	0.04		SERRATIA MARCESCENS AMINOGLYCOSIDE-3-N-CHAIN: A, B;	TRANSFERASE AMINOGLYCOSIDE 3-N-ACETYLTRANSFERASE, EUBACTERIAL 2 AMINOGLYCOSIDE RESISTANCE, GCN5-RELATED N-ACETYLTRANSFERASE, 3 COA-BINDING
1580	1c3w	A	610	732	1.5e-18	0.59	0.63		SEROTONIN N-ACETYLTRANSFERASE; CHAIN: A;	TRANSFERASE N-ACETYLTRANSFERASE
1580	1em0	B	637	751	1e-17	0.13	0.10		P300/CBP ASSOCIATING FACTOR; CHAIN: B, A;	SIGNALING PROTEIN P300/CBP ASSOCIATED FACTOR, COENZYME A, ACETYLTRANSFERASE, 2 COACTIVATOR, SIGNALING PROTEIN
1580	1qsm	A	615	729	3.4e-11	0.17	0.64		HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE
1580	1qsm	A	642	738	1.5e-14	0.08	0.00		HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE
1580	1q4t	A	657	749	8.5e-16	-0.21	0.48		TCF15 HISTONE ACETYLTRANSFERASE; CHAIN: A;	TRANSFERASE HISTONE ACETYLTRANSFERASE, GCN5-RELATED N-ACETYLTRANSFERASE, 2 COA-BINDING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1580	1ygh	A	637	749	5.1e-14	-0.37	0.39		TRANSCRIPTIONAL ACTIVATOR GCN5; CHAIN: A, B;	GENE REGULATION ADA4; TRANSCRIPTIONAL REGULATION, HISTONE ACETYLATION, N-2 ACETYLTRANSFERASE GCN5 RELATED N-ACETYLTRANSFERASE FAMILY, 3 GENE REGULATION
1582	1aog	A	65	116	1.2e-06	0.06	0.21		TRYPTOPHANE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE TRYPTOPHANE REDUCTASE, FAD DEPENDENT DISULPHIDE 2
1582	1b37	A	70	104	0.00014	0.02	0.09		POLYAMINE OXIDASE; CHAIN: A, B, C;	OXIDOREDUCTASE OXIDOREDUCTASE FLAVIN-DEPENDENT AMINE OXIDASE, OXIDOREDUCTASE
1582	3lad	A	67	123	1.5e-07	0.01	0.16		OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	
1587	1b34	A	44	126	1.4e-13	0.48	0.63		SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1; CHAIN: A; SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2; CHAIN: B;	RNA BINDING PROTEIN SNRNP, SPLICING, SPLICEOSOME, SM, CORE SNRNP DOMAIN, 2 SYSTEMIC LUPUS ERYTHEMATOSUS, SLE
1587	1b34	B	40	122	3.4e-11	0.50	0.93		SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1; CHAIN: A; SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2; CHAIN: B;	RNA BINDING PROTEIN SNRNP, SPLICING, SPLICEOSOME, SM, CORE SNRNP DOMAIN, 2 SYSTEMIC LUPUS ERYTHEMATOSUS, SLE
1587	1d3b	A	41	126	1.7e-11	0.50	0.33		SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN	RNA BINDING PROTEIN D3 CORE SNRNP PROTEIN; B CORE SNRNP PROTEIN SNRNP, SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, SLE,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ASSOCIATED CHAIN: B, D, F, H, J, L;	RNA BINDING PROTEIN
1587	1d3b	B	43	134	5.1e-24	0.25	0.99		SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED CHAIN: B, D, F, H, J, L;	RNA BINDING PROTEIN D3 CORE SNRNP PROTEIN; B CORE SNRNP PROTEIN SNRNP; SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, SLE, RNA BINDING PROTEIN
1587	1d3b	D	39	134	8.5e-25	0.26	0.69		SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED CHAIN: B, D, F, H, J, L;	RNA BINDING PROTEIN D3 CORE SNRNP PROTEIN; B CORE SNRNP PROTEIN SNRNP; SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, SLE, RNA BINDING PROTEIN
1588	1b8q	A	12	80	3e-14	0.69	0.96		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
1588	1b8q	A	3	110	3.4e-13	0.72	0.82		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
1588	1b9	A	5	86	1.5e-18	0.56	1.00		PSD-95; CHAIN: A; CRPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
1588	1i16		9	96	1.5e-16	0.35	0.76		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LIG; CYTOKINE, LYMPHOCYTE
1588	1kwa	A	9	82	7.5e-15	0.83	0.93		HCAS/LIN-2 PROTEIN; CHAIN: A, B;	CHEMOKINE/ATTRACTANT FACTOR, PDZ DOMAIN KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDÉCAN, RECEPTOR CLUSTERING, KINASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1588	1pdr		3	90	1e-17	0.78	1.00		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
1588	1qau	A	12	96	1.2e-14	0.89	0.95		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	OXIDOREDUCTASE BETA-FINGER
1588	1qv	A	3	81	3.4e-19	0.66	1.00		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
1588	1qlc	A	1	83	1.4e-15	0.79	0.99		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
1588	3pdz	A	3	86	1.7e-16	0.91	1.00		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING
1590	1e06	A	91	187	8.5e-34	0.36	0.89		GOLGI-ASSOCIATED ATPASE ENHANCER OF 16 KD; CHAIN: A, B;	PROTEIN BINDING GATE-16; UBIQUITIN FOLD
1591	1avl	A	29	244	4.5e-06			34.19	APOLIPOPROTEIN A4; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-1; LIPOPROTEIN LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
1591	1eun	A	28	248	1.5e-07			61.70	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T-AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1591	1dn1	B	17	233	3.4e-22	-0.00	0.45		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1591	1dn1	B	19	233	1.5e-38	0.16	0.95		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1591	1ffo	A	22	213	3.4e-13	0.23	0.04		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1591	1quu	A	28	251	4.5e-12			57.26	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1591	1sc6	B	174	245	9e-24			35.15	SYNAPTOSOMAL VAMP 2; E, I; SYNTAXIN 1A; CHAIN: B; F, I; SNAP-25B; CHAIN: C, G, K; SNAP-25B; CHAIN: D, H, L;	TRANSPORT PROTEIN VAMP 2; MEMBRANE FUSION PROTEIN, COMPLEX, TRANSPORT PROTEIN
1591	4bb1		30	73	5.1e-05	0.49	0.16		DHP1; CHAIN: NULL;	DESIGNED HELICAL BUNDLE
1591	4bb1		36	75	3.4e-05	0.17	0.17		DHP1; CHAIN: NULL;	DESIGNED HELICAL BUNDLE
1592	1aut	L	249	324	1e-10	0.21	0.06		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1592	1aut	L	306	385	4.5e-12	0.32	0.47		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Bias	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1592	1coj	A	246	326	1.5e-09	0.18	0.04		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	COMPLEX (BLOOD COAGULATION/INHIBITOR) SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1592	1cej	A	280	374	1.5e-14	0.06	0.04		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1592	1dam	L	109	186	1.4e-09	0.44	0.09		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DIFFROMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1592	1dam	L	139	249	3.4e-11	0.17	-0.19		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DIFFROMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1592	1dam	L	253	385	3e-15	0.02	0.16		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DIFFROMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)



SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1592	1dva	L	109	186	1.4e-09	0.24	-0.03		DES-GLA FACTOR VIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1592	1dva	L	139	249	3.4e-11	0.13	-0.18		DES-GLA FACTOR VIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1592	1dx5	I	295	383	1.2e-14	-0.18	0.01		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N; O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L- ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1592	1dx5	I	307	402	8.5e-12	0.03	-0.15		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N; O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L- ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1592	1ernn		245	339	1.7e-09	0.01	-0.05		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE

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1592	1emn		277	382	1.7e-15			56.86	FIBRILLIN; CHAIN: NULL;	DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1592	1emn		302	380	1.7e-15	0.33	0.55		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1592	1emn		337	402	8.5e-14	0.36	0.13		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1592	1ext	A	194	357	3e-10			55.46	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
1592	1fk	L	109	186	1.4e-09	0.10	0.03		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR;	BLOOD CLOTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: T; 5L15; CHAIN: I;	RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
1592	1fk6	L	139	249	3.4e-11	0.08	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	COMPLEX/SERINE PROTEASE/COFACTOR/LIGAND, BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
1592	1lgr	A	246	380	4.5e-12	0.20	0.00		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
1592	1klo		112	242	3.4e-13	0.15	0.31		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1592	1klo		146	281	3.4e-18	0.44	-0.12		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1592	1klo		147	331	7.5e-19	0.29	-0.14		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1592	1klo		230	382	3.4e-17	0.19	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1592	1klo		231	396	7.5e-19			70.13	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1592	1klo		27	193	3.4e-12	0.37	-0.14		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1592	1klo		295	403	1e-11	0.07	-0.19		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1592	1pk6	L	109	173	3.4e-09	0.58	-0.12		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1592	1pk6	L	139	229	1.5e-10	0.44	-0.07		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION; 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1592	1qik	L	109	186	1.4e-09	0.55	-0.09		COAGULATION FACTOR VILA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VILA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1592	1qik	L	143	249	3.4e-10	0.23	-0.17		COAGULATION FACTOR VILA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VILA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1592	1qik	L	253	338	7.5e-09	0.26	-0.18		COAGULATION FACTOR VILA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VILA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1592	1qik	L	283	385	1.3e-11	0.49	0.71		COAGULATION FACTOR VILA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VILA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1592	1tng		128	180	3e-10	0.91	-0.05		T-PLASMINOGEN ACTIVATOR FLG; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
1592	1xka	L	109	189	3.4e-09	0.23	-0.12		BLOOD COAGULATION FACTOR XA; CHAIN: L; C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD

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1592	1xka	L	255	328	7.5e-09	0.04	-0.03		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1592	1xka	L	283	382	1.2e-11	0.43	0.46		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1592	1xka	L	305	395	1.2e-11			53.26	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1592	9wga	A	114	264	3.4e-14	0.22	-0.12		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1592	9wga	A	152	340	1.5e-16			60.84	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1592	9wga	A	183	342	1.4e-15	0.04	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1592	9wga	A	92	221	3.4e-13	-0.00	-0.03		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1593	1ba0		1	77	3.4e-28			81.78	DNA; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Bias	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1593	1bq0		3	68	3.4e-28	0.84	1.00		DNAI; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
1593	1hdj		2	78	1e-33			86.98	HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1;
1593	1hdj		3	68	3.4e-27	0.97	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE
1593	1hdj		3	77	1e-33	0.97	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1;
1594	1hme		351	416	1.4e-21	-0.13	0.43		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGCB) (DNA-BINDING HEME 3 HMG-BOX DOMAIN B OF RAT HMG1) (NMJR, 1 STRUCTURE) HME 4	MOLECULAR CHAPERONE
1594	1hry	A	350	416	1e-27	0.01	0.24		HUMAN SRY; IHRY 6 CHAIN: A; IHRY 7 DNA; IHRY 9 CHAIN: B; IHRY 10	COMPLEX (DNA-BINDING PROTEIN/DNA)
1594	1hsm		351	419	3.4e-22	0.11	0.75		DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMG1) BOX 2, COMPLEXED WITH 1HSM 3 MERCAPTOETHANOL (CMR, MINIMIZED AVERAGE STRUCTURE) 1HSM 4	
1594	2lef	A	344	429	3e-22			123.69	LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG; TCR-A; TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
1594	2lef	A	345	420	3e-22	0.31	1.00		LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG; TCR-A;

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1594	2lef	A	350	420	3.4e-20	0.40	1.00		DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
									LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A; TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
1598	1eg7	A	31	106	8.5e-21	0.10	0.89		NON HISTONE PROTEIN 6 A;	DNA BINDING PROTEIN HMG BOX, DNA BINDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
1598	1lry	A	43	114	1e-21	-0.10	0.78		HUMAN SRY; ITRY 6 CHAIN: A; ITRY 7 DNA; ITRY 9 CHAIN: B; ITRY 10	COMPLEX (DNA-BINDING PROTEIN/DNA)
1598	1lry	A	43	115	7.5e-27			83.75	HUMAN SRY; ITRY 6 CHAIN: A; ITRY 7 DNA; ITRY 9 CHAIN: B; ITRY 10	COMPLEX (DNA-BINDING PROTEIN/DNA)
1598	1lry	A	44	115	7.5e-27	0.04	0.81		HUMAN SRY; ITRY 6 CHAIN: A; ITRY 7 DNA; ITRY 9 CHAIN: B; ITRY 10	COMPLEX (DNA-BINDING PROTEIN/DNA)
1598	2lef	A	43	128	6e-27			57.47	LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A; TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
1598	2lef	A	44	128	8.5e-17	-0.29	0.74		LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A; TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING,

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1598	2lef	A	45	116	6e-27	0.27	0.71		LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A; DNA (5'-CHAIN: B; DNA (5'-CHAIN: C;	COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA, GENE REGULATION/DNA, GENE REGULATION/DNA, LEF-1 HMG, LEF1, HMG, TCR, A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
1599	2trc	P	9	173	1.5e-09	0.10	-0.20		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
1602	1e0l	A	133	160	5.1e-07	0.60	0.96		FORMIN BINDING PROTEIN; CHAIN: A;	SH3 DOMAIN WW DOMAIN, FRP28, SIGNAL TRANSDUCTION
1602	1e0l	A	133	161	1.5e-09	0.72	0.94		FORMIN BINDING PROTEIN; CHAIN: A;	SH3 DOMAIN WW DOMAIN, FRP28, SIGNAL TRANSDUCTION
1602	1e0l	A	87	121	3e-09	0.17	0.90		FORMIN BINDING PROTEIN; CHAIN: A;	SH3 DOMAIN WW DOMAIN, FRP28, SIGNAL TRANSDUCTION
1602	1e0l	A	92	121	8.5e-08	0.09	0.98		FORMIN BINDING PROTEIN; CHAIN: A;	SH3 DOMAIN WW DOMAIN, FRP28, SIGNAL TRANSDUCTION
1602	1e0m	A	129	159	3.4e-09	0.03	0.87		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
1602	1e0m	A	85	118	3.4e-12	0.64	0.35		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
1602	1eg3	A	82	117	3.4e-06	0.27	0.22		DYSTROPHIN; CHAIN: A;	STRUCTURAL PROTEIN EF-HAND LIKE DOMAIN, WW DOMAIN



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1602	1l8a	B	132	185	6e-06	-0.06	0.01		PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA- CHAIN: B; YSEP/PT(SEP/S PEPTIDE; CHAIN: C;	ISOMERASE PINI; PEPTIDYL-PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING
1603	1e0l	A	90	125	1e-07	-0.19	0.82		FORMIN BINDING PROTEIN; CHAIN: A;	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION
1603	1e0l	A	96	124	1.5e-09	0.72	0.94		FORMIN BINDING PROTEIN; CHAIN: A;	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION
1603	1e0m	A	96	121	6.8e-05	0.25	0.99		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
1603	1e0m	A	96	121	6e-05	0.25	0.99		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
1603	1l8a	B	95	148	6e-06	-0.06	0.01		PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA- CHAIN: B; YSEP/PT(SEP/S PEPTIDE; CHAIN: C;	ISOMERASE PINI; PEPTIDYL-PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING
1606	1b14	A	1	387	1.7e-67	0.20	0.78		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A;	TRANSFERASE TRANSFERASE, METABOLIC ROLE, PYRIDOXAL 5'-PHOSPHATE
1606	1b1n	A	26	389	1.7e-58			355.62	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE PSAT; BIOSYNTHESIS
1606	1b1n	A	27	389	1.7e-58	0.71	1.00		PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE PSAT; BIOSYNTHESIS
1606	1b14	A	26	389	5.1e-60	0.84	1.00		PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A;	TRANSFERASE PSAT; AMINOTRANSFERASE, PYRIDOXAL-5-PHOSPHATE, PHOSPHOSERINE, 2 ALKALIPHILIC
1606	1c0n	A	11	389	1.7e-61	0.28	1.00		CSDB PROTEIN; CHAIN: A;	LYASE ALPHA/BETA FOID
1606	1c0j	A	1	387	5.1e-67	0.07	0.59		SERINE HYDROXYMETHYLTRANSFERASE	TRANSFERASE SHMT; HYDROXYMETHYL TRANSFERASE,

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1606	1dfo	A	8	386	1.7e-67	0.11	0.66		ASE; CHAIN: A, B; SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D; ASPARTATE, AMINO TRANSFERASE, (AA/T)-LIKE FOLD	I CARBON METABOLISM TRANSFERASE SHMT; SERINE METHYLASE; ALPHA PLP TRANSFERASE SHMT; SERINE- PYRIDOXAL 5'-PHOSPHATE, 2 TETRAHYDROFOLATE, ASYMMETRIC DIMER
1606	1eji	A	1	386	1.7e-66	-0.02	0.42		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D; ASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT; SERINE- PYRIDOXAL 5'-PHOSPHATE, 2 TETRAHYDROFOLATE, ASYMMETRIC DIMER
1607	1bj4	A	1	344	3.4e-62	0.15	0.18		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A; PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE, METABOLIC ROLE, PYRIDOXAL 5'- PHOSPHATE AMINOTRANSFERASE PSAT; AMINOTRANSFERASE, L-SERINE BIOSYNTHESIS
1607	1bjn	A	26	343	1.7e-49			282.66	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B; PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B; PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A;	AMINOTRANSFERASE PSAT; BIOSYNTHESIS AMINOTRANSFERASE PSAT; AMINOTRANSFERASE, L-SERINE BIOSYNTHESIS TRANSFERASE PSAT; AMINOTRANSFERASE, PYRIDOXAL-5'-PHOSPHATE, PHOSPHOSERINE, 2 ALKALIPHILIC LYASE ALPHA/BETA FOLD
1607	1edn	A	11	344	8.5e-56	-0.01	0.48		CSDR PROTEIN; CHAIN: A; SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE SHMT; HYDROXYMETHYL TRANSFERASE, I CARBON METABOLISM
1607	1ej0	A	1	344	6.8e-62	-0.04	0.43		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D; ASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT; SERINE METHYLASE; ALPHA PLP ASPARTATE, AMINO TRANSFERASE SHMT; SERINE- GLYCINE CONVERSION,
1607	1dfo	A	3	344	5.1e-66	0.07	-0.02		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D; ASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT; SERINE- GLYCINE CONVERSION,
1607	1eji	A	1	344	5.1e-59	0.07	0.07		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D; ASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT; SERINE- GLYCINE CONVERSION,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ASE; CHAIN: A, B, C, D;	PYRIDOXAL 5'-PHOSPHATE, 2 TETRAHYDROFOLATE, ASYMMETRIC DIMER
1608	1bg1	A	1	70	0.00051	-0.48	0.04		STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	COMPLEX (TRANSCRIPTION FACTOR) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION FACTOR) DNA
1608	1fkk	A	1	82	1.2e-06	-0.33	0.11		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAL PROTEIN
1609	1quu	A	96	345	7.5e-05			70.36	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1612	1ctc		552	603	3.4e-11	-0.23	0.01		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1612	1fbv	A	515	611	0.003	-0.31	0.22		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBC17; CHAIN: C;	LIGASE CBL, UBC17, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
1614	1b0x	A	828	885	6.8e-14	0.02	0.04		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE

SEQ ID NO	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1614	1b4f	A	825	885	6.8e-15	0.21	-0.09		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	SIGNAL TRANSDUCTION SAM DOMAIN; EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER
1616	1a25	A	588	716	1.5e-26	0.08	1.00		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM4+PHOSPHOLIPID-BINDING PROTEIN; 2 CALCIUM-BINDING PROTEIN
1616	1a25	A	728	864	4.5e-16	0.32	1.00		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM4+PHOSPHOLIPID-BINDING PROTEIN; 2 CALCIUM-BINDING PROTEIN
1616	1a25	A	755	871	1.5e-36	0.33	0.37		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM4+PHOSPHOLIPID-BINDING PROTEIN; 2 CALCIUM-BINDING PROTEIN
1616	1byn	A	588	717	3e-28	-0.05	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1616	1byn	A	618	721	1.2e-08	-0.02	0.59		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1616	1byn	A	732	856	6.8e-22	0.85	0.89		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1616	1dix	A	606	699	1.5e-14	-0.50	0.00		PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE C; CHAIN: B;	LIPID DEGRADATION PLC- $\beta$ ; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.A.A	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
										DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1616	1dqy	A	587	875	8.5e-59	0.13	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1616	1dsy	A	588	716	1.2e-27	-0.11	1.00		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1616	1dsy	A	728	845	4.5e-14	0.20	0.99		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1616	1dsy	A	751	872	1.7e-39	0.12	0.17		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1616	1rlw		606	726	9e-20	-0.09	0.58		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1616	1rsy		588	717	6e-30	0.12	1.00		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1616	1rsy		732	856	6.8e-22	0.39	0.59		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1616	3rpb	A	730	874	3.4e-46	0.07	0.36		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										DOMAINS, C2B-DOMAIN, RAPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1617	1a25	A	230	351	6.8e-27	0.28	0.34		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM4-H/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1617	1a25	A	69	197	1.5e-26	0.08	1.00		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM4-H/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1617	1a25	A	69	208	1.5e-26			59.65	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM4-H/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1617	1byn	A	221	343	6.8e-23	0.26	0.21		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCTOSIS/EXOCYTOSIS
1617	1byn	A	69	196	1.7e-27	0.33	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCTOSIS/EXOCYTOSIS
1617	1byn	A	69	198	3e-28	-0.05	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCTOSIS/EXOCYTOSIS
1617	1qy	A	230	333	1.7e-16	0.13	-0.05		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	ENDOCTOSIS/EXOCYTOSIS

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1617	1cqv	A	71	356	3.4e-52	-0.26	0.39		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1617	1dsy	A	232	351	1.2e-28	0.24	0.13		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1617	1dsy	A	68	203	3.4e-21	-0.23	0.70		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1617	1dsy	A	69	197	1.2e-27	-0.11	1.00		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1617	1rlw		87	207	9e-20	-0.09	0.58		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; CALB DOMAIN
1617	1rsy		221	343	6.8e-23	0.16	0.07		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1617	1rsy		62	200	6e-30			69.42	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1617	1rsy		69	196	1.7e-27	0.39	1.00		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1617	1rsy		69	198	6e-30	0.12	1.00		CALCIUM/PHOSPHOLIPID	





SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Binst	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYEOCYTIC LEUKEMIA, GENE REGULATION
1620	1dsx	A	3	89	3.4e-25	0.28	0.99		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D, E, F, G, H;	SIGNALING PROTEIN VOLTAGE- GATED POTASSIUM CHANNEL, ASSEMBLY DOMAIN, TETRAMER
1620	1exb	E	2	92	1.5e-26	0.31	0.99		KV BETA2 PROTEIN; CHAIN: A; POTASSIUM CHANNEL KV1.1; CHAIN: E;	METAL TRANSPORT ION CHANNEL, OXIDOREDUCTASE, BETA SUBUNIT
1620	1qdv	A	3	101	1.7e-26	-0.10	0.82		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D;	SIGNALING PROTEIN VOLTAGE- GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER
1620	1i1d	A	3	101	1.2e-26	0.38	0.95		POTASSIUM CHANNEL KV1.1; CHAIN: A;	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY STRUCTURE, 2 APLYSIA KV1.1, PROTON TRANSPORT
1620	3kvt		2	102	8.5e-29	0.55	1.00		POTASSIUM CHANNEL PROTEIN SHA W; CHAIN: NULL;	POTASSIUM CHANNEL, POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC-BINDING
1621	1cum	A	17	158	0.003	-0.18	0.01		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2, 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1621	1cum	A	1	212	0.003			53.11	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1623	1bu2	A	52	149	1.4e-19	0.05	0.37		CYCLIN HOMOLOG; CHAIN: A;	CELL CYCLE REGULATION CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL CYCLIN
1623	1jkw		78	148	1.2e-12	0.03	0.30		CYCLIN H; CHAIN: NULL;	CELL DIVISION RCYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN
1623	1qmr	B	41	148	8.5e-42	0.33	0.76		CELL DIVISION PROTEIN KINASE 2; CHAIN: A, C; G2/MITOTIC-SPECIFIC CYCLIN A; CHAIN: B, D; SUBSTRATE PEPTIDE; CHAIN: E, F;	COMPLEX (PROTEIN KINASE/CYCLIN) CYCLIN-DEPENDENT KINASE-2, CDK2, P33 PROTEIN KINASE, CCNA, CCN1; COMPLEX (PROTEIN KINASE/CYCLIN), CYCLIN, CDK, 2 PHOSPHORYLATION, SUBSTRATE COMPLEX
1623	1vin		47	148	1.7e-40	0.40	0.77		CYCLIN A; CHAIN: NULL;	BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY-SUBUNIT, 2 BINDING PROTEIN
1624	1alh	A	110	169	1.2e-19	0.35	0.84		QOSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1624	1alh	A	33	134	6.8e-22	-0.10	0.89		QOSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1624	1alh	A	70	165	1.4e-25	-0.01	0.70		QOSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Ts Blast	Verily score	PMF score	SEQFOL D score	Compound	PDB annotation
1624	1mcy	C	109	169	3.4e-33	0.35	0.92		SITE; CHAIN: B, C; DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	PROTEIN COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1624	1mcy	C	33	134	1.7e-41	-0.29	0.46		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1624	1mcy	C	68	165	3.4e-45	0.06	0.75		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1624	1mcy	C	68	166	3.4e-45			58.17	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1624	1mcy	C	7	93	6.8e-38	-0.00	0.18		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1624	1mcy	G	107	134	1.5e-13	0.08	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1624	1mcy	G	135	165	1.5e-11	0.44	0.06		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1624	1uf3	A	110	169	1e-14	0.43	0.12		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMJ, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1624	1uf3	A	69	165	3.4e-17	-0.23	0.25		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMJ, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1624	1ubd	C	117	169	1.7e-13	0.21	-0.02		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1624	1ubd	C	30	166	5.1e-28			51.82	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ NO:	PDB ID	CHAI ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1624	1ubd	C	39	165	5.1e-28	-0.13	0.42		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1624	2adr		110	167	3.4e-15	-0.20	0.63		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1624	2drp	A	105	165	1e-09	0.14	0.29		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1624	2gii	A	13	164	6.8e-25	0.03	0.10		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1624	2gii	A	76	169	8.5e-21	0.01	0.09		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1627	1b8q	A	56	186	4.5e-19			54.14	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
1627	1b8q	A	65	181	4.5e-19	0.83	0.84		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
1627	1be9	A	48	170	1.5e-14			52.53	PSD-95; CHAIN: A; CRIFT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsl Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1627	1be9	A	98	153	1.5e-14	0.12	0.24		PSD-95; CHAIN: A; CRPT; CHAIN: B;	LOCALIZATION PEPTIDE RECOGNITION PEPTIDE RECOGNITION PROTEIN LOCALIZATION
1627	1h16		35	161	3e-22			70.34	INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1627	1h16		67	157	3e-22	0.39	0.76		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1627	1kwa	A	67	149	3e-19	0.55	0.98		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT; DHR; PDZ DOMAIN; NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE OXIDOREDUCTASE BETA-FINGER
1627	1qau	A	67	176	1.2e-20	0.47	0.37		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
1627	1qav	A	67	149	6e-20	1.02	1.00		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	
1627	1qlc	A	67	149	3e-22	0.75	1.00		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN; NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
1627	1qlc	A	85	143	1.5e-15	0.05	0.17		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN; NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
1627	3pdz	A	56	143	1.7e-17	0.30	0.65		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS,







SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* O, P, Q, R, S, T; POLYDENYLATE BINDING	BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1629	1evj	H	70	209	1.4e-31			33.52	PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* O, P, Q, R, S, T; POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1629	1evj	H	71	202	8.5e-27	0.35	1.00		PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* O, P, Q, R, S, T; POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1629	1evj	H	72	209	1.4e-31	0.51	0.99		PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* O, P, Q, R, S, T; POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1629	1ha1		52	144	3.4e-25	0.69	1.00		HNRNP A1; CHAIN: NULL; NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN HNRNP, RBD, RRM, ENP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN HNRNP, RBD, RRM, ENP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1629	1ha1		65	229	3.4e-56	1.05	1.00		HNRNP A1; CHAIN: NULL; NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN HNRNP, RBD, RRM, ENP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN HNRNP, RBD, RRM, ENP, RNA BINDING, 2 RIBONUCLEOPROTEIN

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1629	1ha1		66	230	3.4e-56			167.63	HNRP A1; CHAIN: NULL;	RIBONUCLEOPROTEIN NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; NUCLEAR PROTEIN, HNRP, RBD, RMA, RNP, RNA BINDING, 2
1629	1hd1	A	71	144	3.4e-27	1.26	1.00		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RIBONUCLEOPROTEIN RNA BINDING PROTEIN RNA- BINDING DOMAIN
1629	1hd1	A	71	145	1.5e-27	1.29	1.00		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1629	1osm	A	235	329	1.5e-11	1.27	-0.19		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
1629	1pho		241	324	1.5e-11	1.08	-0.19		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) IPHO 3	
1629	1qm9	A	22	145	6e-17	0.55	0.23		POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
1629	1sxl		61	150	6e-25	0.66	0.60		RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS OF SECOND RNA- BINDING DOMAIN) ISXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) ISXL 4 (NMK, 17 STRUCTURES) ISXL 5	
1629	1sxl		62	150	1.7e-16	0.71	0.45		RNA-BINDING PROTEIN SEX-	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Binst	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN ISXL 3 (RBD-2), RESIDUES 199-294 PLUS N-TERMINAL MET) ISXL 4 (NMR, 17 STRUCTURES) ISXL 5	
1629	2omf		237	328	9e-13	1.23	-0.20		MATRIX PORIN OUTER MEMBRANE PROTEIN F; 2OMF 5 CHAIN: NULL; 2OMF 6	INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN, 2OMF 7 PORIN, MEMBRANE PROTEIN 2OMF 12
1629	2up1	A	52	144	1e-28	1.05	1.00		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1629	2up1	A	64	233	5.1e-57	1.18	1.00		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1629	2up1	A	64	239	5.1e-57			165.44	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1629	3ax1	A	69	229	5.1e-36			70.15	SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RCM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1629	3xcl	A	70	229	5.1e-36	0.88	1.00		SEX-LETHAL; CHAIN: A, B, C;	DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD; RNA RECOGNITION MOTIF, RRM, 2 SPICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1635	1e0f	I	47	84	0.006	0.77	0.98		THROMBIN; CHAIN: A,B,C; THROMBIN; CHAIN: D,E,F; HAEMADIN; CHAIN: I,L,K;	COAGULATION/CRYSTAL STRUCTURE/HEPARIN-B FACTOR IIA: COAGULATION/CRYSTAL STRUCTURE/HEPARIN-BINDING SITE/2 HIRUDIN/THROMBIN INHIBITOR
1637	1d0n	A	5	715	0	0.81	1.00		HORSE PLASMA GELSOLIN; CHAIN: A, B	CONTRACTILE PROTEIN MIXED ALPHA-BETA STRUCTURE, ACTIN-BINDING PROTEIN, PROTEIN 2 DOMAIN PACKING, CONTRACTILE PROTEIN
1637	1d0n	A	5	715	0			876.96	HORSE PLASMA GELSOLIN; CHAIN: A, B	CONTRACTILE PROTEIN MIXED ALPHA-BETA STRUCTURE, ACTIN-BINDING PROTEIN, PROTEIN 2 DOMAIN PACKING, CONTRACTILE PROTEIN
1641	1akh	A	90	130	6e-06	0.54	0.95		MATING-TYPE PROTEIN A-1; CHAIN: A; MATING-TYPE PROTEIN ALPHA-2; CHAIN: B; DNA; CHAIN: C;	COMPLEX (TWO DNA-BINDING PROTEINS/DNA) MAT ALPHA-2; COMPLEX (TWO DNA-BINDING PROTEINS/DNA), COMPLEX, 2 DNA-BINDING PROTEIN, DNA, TRANSCRIPTION REGULATION

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsl Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1641	1au7	A	92	134	7.5e-06	0.22	0.55		PTT-1; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA); PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR
1641	1b72	B	92	136	1.5e-05	-0.02	0.33		HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; CHAIN: E; INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1641	1bw5		92	134	1.5e-06	0.17	0.49		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	DNA-BINDING PROTEIN ISL-1HD
1641	1fjl	A	92	134	1.2e-05	0.89	0.98		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN
1641	1fjl	B	92	134	9e-06	0.71	0.98		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1641	1hdp		83	134	6e-06	0.33	0.69		DNA-BINDING PROTEIN OCT-2 POU HOMEODOMAIN (NMR, AVERAGE STRUCTURE) 1HDP	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1641	1ocp		92	134	1.3e-06	0.66	0.62		OCT-3; 1OCT 5 CHAIN: NULL; 1OCT 6	DNA-BINDING PROTEIN
1641	1pog		83	134	3e-06	0.46	0.78		DNA BINDING PROTEIN OCT-1 POU HOMEODOMAIN DNA-BINDING PROTEIN MUTANT WITH IPOG 3 ARG GLY SER HIS MET INSERTED AT THE N-TERMINUS AND ASP ILE IPOG 4 INSERTED AT THE C-TERMINUS (NMR/RSSEM-R6,INSU166-D) IPOG 5 (NMR,	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									13 STRUCTURES) IPOG 6	
1653	1lpb	A	29	64	8e-19	-0.36	0.81		HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	
1653	1lpb	A	29	65	3e-20	-0.35	0.88		HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	
1653	1lpb	A	8	66	3e-20			30.95	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	
1653	1pen		29	69	3.2e-20	-0.36	1.00		LIPASE PROTEIN COFACTOR PORCINE PANCREATIC PROCOLIPASE B IPCN 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IPCN 4	
1653	1pen		29	69	6e-22	-0.36	1.00		LIPASE PROTEIN COFACTOR PORCINE PANCREATIC PROCOLIPASE B IPCN 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IPCN 4	
1653	1pen		2	69	6e-22			56.60	LIPASE PROTEIN COFACTOR	

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PORCINE PANCREATIC PROCOLIPASE B IPCN 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IPCN 4	
1654	1a09	A	1	99	3.2e-28	-0.10	0.03		C-SRC TYROSINE KINASE; CHAIN: A; B: ACB-FORMYL PHOSPHOTYR-GLU-(NN-DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
1654	1bkl		1	102	3.2e-29	-0.06	0.06		PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN
1654	1bij		1	99	3.2e-27	-0.37	0.11		P55 BLK PROTEIN TYROSINE KINASE; CHAIN: NULL;	PHOSPHORYLATION SIGNAL TRANSDUCTION TYROSINE KINASE, TRANSFERASE, 2 PHOSPHOTRANSFERASE, PHOSPHORYLATION
1654	1ddm	A	120	247	3e-17	0.08	0.95		NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	SIGNALING PROTEIN/TRANSFERASE NAK; COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMMETRIC CELL DIVISION
1654	1fmk		1	165	3.2e-44	-0.32	0.01		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1654	1sha	A	1	99	9.6e-29	-0.17	0.04		PHOSPHOTRANSFERASE V-SRC TYROSINE KINASE	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									TRANSFORMING PROTEIN (PHOSPHOTYROSINE ISHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.12) COMPLEX WITH ISHA 4 PHOSPHOPEPTIDE A (TYR-VAL-PRO-MET-LEU; PHOSPHORYLATED TYR) ISHA 5	
1654	1shc	A	110	247	0.00075	0.17	0.10		SHC; CHAIN: A; TRKA RECEPTOR PHOSHOPEPTIDE; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE); COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE); PHOSPHOTYROSINE 2 BINDING DOMAIN (PTB)
1654	2mb	A	108	247	9e-24	0.21	0.93		NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION; PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION
1654	2mb	A	108	248	9e-24			51.48	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION; PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION
1654	2mb	A	110	260	0.00032	0.34	0.98		NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION; PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										REGULATION
1658	2ifl		29	149	1.6e-44			141.21	EIF1 CHAIN: NULL;	TRANSLATION INITIATION FACTOR SUI1; TRANSLATION INITIATION FACTOR
1658	2ifl		42	149	1.6e-44	0.42	1.00		EIF1 CHAIN: NULL;	TRANSLATION INITIATION FACTOR SUI1; TRANSLATION INITIATION FACTOR
1660	1d2n	A	186	257	1.6e-11	-0.15	0.36		N-ETHYLMALIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN
1660	1g4l	A	140	260	1.3e-17	-0.14	0.13		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
1663	1fmlk		334	426	4.8e-22	-0.13	0.45		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC, SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1663	1gbq	A	335	386	9.6e-15	0.09	0.17		GRB2; CHAIN: A; SOS-1; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN
1663	1gbr	A	335	392	1.6e-15	0.09	0.59		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL IGBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE IGBR 4 (NMR, 29 STRUCTURES) IGBR 5	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1663	1gfc		333	389	6.4e-15	0.40	0.83		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BINDING PROTEIN 2 (GRB2) IGRC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) IGFC 4	
1663	1gri	A	304	389	6.4e-16	-0.64	0.35		GROWTH FACTOR BOUND PROTEIN 2; IGRI 5 CHAIN: A, B; IGRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 IGRI 14
1663	1lck	A	334	425	1.4e-18	0.30	0.28		P56-LCK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL- PHOSHOPEPTIDE TEGQPHOSPHOYQPPA; ILCK 14 CHAIN: B; ILCK 15	COMPLEX (KINASE/PEPTIDE)
1663	1qcf	A	333	426	1.6e-21	0.20	0.09		HAEMATOPoETIC CELL KINASE (LCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1663	1sem	A	330	389	1.6e-16	0.43	0.96		SEM-5; ISEM 3 CHAIN: A, B; ISEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS ISEM 8 CHAIN: C, D ISEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, ISEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR ISEM 19
1663	2abl		327	426	4.8e-16	0.03	-0.06		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
1669	1ee4	A	36	416	3e-05	0.09	0.41		KARYOPHERIN ALPHA1; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE 1 SUPPRESSOR PROTEIN; ARM REPEAT
1669	2bat		107	530	7.5e-10	0.02	0.10		BETA-CATENIN; CHAIN: NULL;	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										CATENIN, STRUCTURAL PROTEIN
1671	1a4y	A	27	362	6.4e-12	0.16	0.27		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1671	1a4y	A	29	314	1.5e-37	0.54	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1671	1a9n	A	126	301	1.5e-19	0.10	0.40		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1671	1a9n	A	27	131	9.6e-07	0.36	0.74		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1671	1a9n	A	30	171	1e-23	0.41	0.37		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1671	1a9n	A	53	230	1.5e-22	-0.03	0.34		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1671	1a9n	C	126	301	9e-20	0.28	0.82		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1671	1a9n	C	171	299	4.5e-24	0.50	0.60		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1671	1a9n	C	216	342	0.00064	0.13	0.00		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1671	1a9n	C	220	334	9e-18	0.24	0.95		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1671	1a9n	C	27	131	9.6e-07	0.40	0.84		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1671	1a9n	C	30	174	9e-24	0.44	0.01		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1671	1a9n	C	53	240	6e-23	0.16	0.57		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1671	1d0b	A	138	290	1.5e-23	0.70	0.94		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH ADHESION
1671	1d0b	A	173	381	1.6e-21	0.18	0.95		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH ADHESION
1671	1d0b	A	29	106	6e-14	0.31	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH ADHESION
1671	1d0b	A	360	521	8e-21	0.04	-0.19		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH ADHESION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1671	1d0b	A	43	196	1.3e-27	0.74	1.00		INTERNALIN B; CHAIN: A;	REPEAT, CALCIUM BINDING, CELL ADHESION
1671	1d0b	A	70	242	8e-28	0.61	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH ADHESION
1671	1dce	A	145	250	4.8e-14	0.49	1.00		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C, RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1671	1dce	A	1	107	3.2e-06	0.18	0.36		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C, RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1671	1dce	A	27	130	4.8e-10	0.66	1.00		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C, RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1671	1dce	A	43	154	4.8e-12	0.68	0.89		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C, RAB GERANYLGERANYLTRANSFERASE	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1671	1g59	A	154	289	1.6e-13	-0.03	0.11		RASE BETA SUBUNIT; CHAIN: B, D; OUTER ARM DYNEIN; CHAIN: A;	SUBUNIT, BETA SUBUNIT CONTRACTILE PROTEIN LUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1671	1g59	A	165	299	1.4e-21	-0.14	0.69		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1671	1g59	A	201	380	6.4e-10	-0.32	0.01		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1671	1g59	A	27	148	1.6e-12	0.03	0.64		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1671	1g59	A	59	195	3.2e-16	0.09	0.52		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1671	1f88	B	403	702	1.5e-14	-0.04	0.05		RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1671	1fo1	A	27	83	8e-05	0.27	0.72		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LUCINE-RICH-REPEAT 2 (LRR)
1671	1fo1	A	45	107	1.1e-05	-0.08	0.22		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LUCINE-RICH-

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1671	1601	B	45	107	1.1e-05	0.32	0.90		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	REPEAT 2 (LRR) RNA BINDING PROTEIN FAP (NFXD); RIBONUCLEOPROTEIN (RNP_RBD OR RGM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1671	1yrg	A	29	154	1.5e-16	-0.01	0.25		GTPASE-ACTIVATING PROTEIN RNAI_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAI P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SWI; GTPASE-ACTIVATING PROTEIN, GAP, RNAI P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1671	2bnh		29	314	6e-50	0.41	0.68		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1671	2bnh		30	424	1.4e-16	0.19	0.21		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1671	2bnh		99	334	3e-31	0.33	1.00		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1673	1f61	A	90	129	1.6e-08	-0.85	0.34		CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	LIGASE SKP2 F-BOX; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1673	1f61	A	92	129	1.3e-08	-0.62	0.59		CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45;	LIGASE SKP2 F-BOX; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3,

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1673	1b62	A	90	162	6.4e-09	-0.51	0.28		CHAIN: B, D; SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	UBIQUITIN PROTEIN LIGASE LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1675	1bu6	O	18	491	0	0.56	1.00		GLYCEROL KINASE; CHAIN: O, Y, Z, X;	TRANSFERASE ALLOSTERY, COOPERATIVITY, GLYCEROL KINASE, CRYSTAL 2 STRUCTURE, TRANSFERASE
1675	1bu6	O	18	492	0			310.87	GLYCEROL KINASE; CHAIN: O, Y, Z, X;	TRANSFERASE ALLOSTERY, COOPERATIVITY, GLYCEROL KINASE, CRYSTAL 2 STRUCTURE, TRANSFERASE
1676	1aun		1	191	0.009			52.19	PR-5D; CHAIN: NULL;	ANTIFUNGAL PROTEIN OSMOTIN- LIKE PROTEIN; ANTIFUNGAL PROTEIN, PATHOGENESIS- RELATED PROTEIN, PR-5D, 2 OSMOTIN, THAUMATIN-LIKE PROTEIN
1676	1c2a	A	134	201	4.5e-17	-0.16	0.09		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
1676	1c2a	A	42	162	6e-16	1.29	0.00		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
1676	1c2a	A	4	118	6e-15	1.60	-0.14		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
1676	1c2a	A	84	197	3e-19	0.79	-0.18		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1676	1ehd	A	104	192	1.2e-17	0.87	0.01		AGGLUTININ ISOLECTIN VI; CHAIN: A	INHIBITOR PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1676	1ehd	A	10	100	1.2e-19	1.43	-0.14		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1676	1ehd	A	84	172	3e-18	1.28	-0.12		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1676	1eis	A	10	116	1.5e-18	1.17	-0.18		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1676	1eis	A	124	192	1.3e-14	0.05	-0.12		AGGLUTININ ISOLECTIN VI; CHAIN: A	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1676	1eis	A	3	86	7.5e-18	1.32	0.15		AGGLUTININ ISOLECTIN VI; CHAIN: A	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1676	1eis	A	64	142	1.5e-19	1.70	-0.14		AGGLUTININ ISOLECTIN VI; CHAIN: A	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1676	1eis	A	77	172	3e-18	1.37	-0.17		AGGLUTININ ISOLECTIN VI; CHAIN: A	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1676	1em2	A	104	192	1e-18	0.98	-0.14		AGGLUTININ ISOLECTIN VI; CHAIN: A	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1676	1em2	A	10	106	3e-17	1.34	-0.12		AGGLUTININ ISOLECTIN VI; CHAIN: A	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1676	1em2	A	3	86	1.1e-16	1.29	0.15		AGGLUTININ ISOLECTIN VI; CHAIN: A	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	LECTIN, HEVEIN DOMAIN, UDA, SUPRANTIGEN, SACCHARIDE BINDING
1676	1am2	A	74	172	3e-18	1.54	0.01		AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPRANTIGEN, SACCHARIDE BINDING
1676	1ext	A	47	199	3e-15			59.75	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING
1676	1ext	A	49	197	3e-15	0.74	-0.19		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING
1676	1igr	A	10	200	6e-25	0.85	-0.20		INSULIN-LIKE GROWTH FACTOR RECEPTOR I; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
1676	1llo		35	199	3e-25	1.09	0.05		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1676	1llo		3	159	6e-24	1.39	-0.15		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1676	1llo		4	160	3e-25			84.67	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1676	1nef	A	46	200	1e-11			50.00	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE
1676	1osm	A	5	138	4.5e-14	1.37	-0.20		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANS-MEMBRANE
1676	1pfx	L	42	201	4.5e-19	0.33	-0.20		FACTOR IXA; CHAIN: C, L, D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEINASE, CALCIUM-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1676	1qub	A	3	200	1.4e-30	0.83	-0.20		HUMAN BETA-2-GLYCOPROTEIN 1; CHAIN: A;	BINDING, HYDROLASE, 3 GLYCOPROTEIN
1676	1skz		13	168	6e-15	0.92	-0.15		ANTISTASIN; CHAIN: NULL;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTIDOMAIN, MEMBRANE ADHESION SERINE PROTEASE INHIBITOR
1676	1skz		74	175	1.1e-15	1.27	0.29		ANTISTASIN; CHAIN: NULL;	ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1676	1skz		95	198	6e-21	0.53	-0.12		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1676	1skz		93	202	6e-21			60.99	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1676	1vmo	A	1	107	1.5e-14	1.30	-0.20		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1676	9wga	A	8	189	4.5e-23			101.83	IVMO 3 LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1680	1c0p	A	11	39	0.00048	-0.46	0.19		D-AMINO ACID OXIDASE; CHAIN: A;	OXIDOREDUCTASE ALPHA-BETA-ALPHA MOTIF, FLAVIN CONTAINING PROTEIN, OXIDASE
1680	1chu	A	7	46	0.00014	-0.05	0.13		L-ASPARTATE OXIDASE; CHAIN: A;	FLAVOENZYME FLAVOENZYME, NAD BIOSYNTHESIS, FAD, OXIDOREDUCTASE
1680	1c1e	A	10	457	3.2e-37			62.05	ADRENODOXIN REDUCTASE; CHAIN: A;	OXIDOREDUCTASE ADR, NADPH; ADRENODOXIN
									OXIDOREDUCTASE; FLAVOENZYME, NAD ANALYSIS, ELECTRON TRANSFERASE	
1680	1c4d	A	142	318	3.2e-09	-0.03	0.36		FLAVOCYTOCHROME C FUMARATE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE TETRAHEME FLAVOCYTOCHROME C FUMARATE REDUCTASE, 2 OXIDOREDUCTASE
1680	1d1n	A	2	182	1.6e-12	-0.09	0.12		TRIMETHYLAMINE DEHYDROGENASE, CHAIN: A; B;	OXIDOREDUCTASE IRON-SULFUR FLAVOPROTEIN, ELECTRON TRANSFER, OXIDOREDUCTASE
1680	1d1n	A	5	359	9e-13	-0.08	0.70		TRIMETHYLAMINE DEHYDROGENASE, CHAIN: A; B;	OXIDOREDUCTASE IRON-SULFUR FLAVOPROTEIN, ELECTRON TRANSFER, OXIDOREDUCTASE
1680	1dcl	A	2	118	0.003	-0.41	0.00		DIHYDROLIPOAMIDE DEHYDROGENASE, CHAIN: A; B, C, D;	OXIDOREDUCTASE LIPOAMIDE DEHYDROGENASE, L PROTEIN, E3, DLDH, DIHYDROLIPOAMIDE DEHYDROGENASE, MULTIZYME COMPLEX 2 PROTEIN, PYRUVATE DEHYDROGENASE COMPLEX, GLYCINE 3 DECARBOXYLASE COMPLEX, FLAVOPROTEIN

SEQ ID NO:	PDB	CHAI ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1680	1gxl	A	8	462	3.2e-94	-0.07	0.39		DIHYDROLIPOAMIDE DEHYDROGENASE, CHAIN: A, B, C, D;	OXIDOREDUCTASE LIPOAMIDE DEHYDROGENASE, L PROTEIN, E3, DLDH, DIHYDROLIPOAMIDE DEHYDROGENASE, MULTIZENZYME COMPLEX 2 PROTEIN, PYRUVATE DEHYDROGENASE COMPLEX, GLYCINE 3 DECARBOXYLASE COMPLEX, FLAVOPROTEIN COMPLEX
1680	1ebd	A	14	462	1.6e-93	-0.04	0.69		DIHYDROLIPOAMIDE DEHYDROGENASE, CHAIN: A, B; DIHYDROLIPOAMIDE ACETYLTRANSFERASE; CHAIN: C;	(OXIDOREDUCTASE/TRANSFERASE ) EBD, REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE
1680	1f8s	A	6	49	1.6e-07	-0.50	0.04		L-AMINO ACID OXIDASE; CHAIN: A, B, C, D, E, F, G, H;	OXIDOREDUCTASE FLAVOENZYME OXIDASE, ENANTIOMERIC SPECIFICITY, O-2 AMINO BENZOATE, ACTIVE SITE, FUNNEL, HELICAL DOMAIN, PAD-3 BINDING DOMAIN
1680	1fcd	A	10	407	1.6e-19	0.10	0.22		ELECTRON TRANSPORT(FLAVOCYTOCHROME ONE) FLAVOCYTOCHROME C SULFIDE DEHYDROGENASE (FCD) IFCD 3	
1680	1fcd	A	9	394	1.6e-19			83.15	ELECTRON TRANSPORT(FLAVOCYTOCHROME ONE) FLAVOCYTOCHROME C SULFIDE DEHYDROGENASE (FCD) IFCD 3	
1680	1fcc	A	2	118	7.5e-05	0.11	0.51		TRYPANOTHIONE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE REDOX-ACTIVE CENTER, OXIDOREDUCTASE, FLAVOPROTEIN, FAD, NADP
1680	1fcc	A	8	459	1.6e-74	0.00	-0.01		TRYPANOTHIONE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE REDOX-ACTIVE CENTER, OXIDOREDUCTASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fs Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1680	1foh	A	12	43	0.00032	-0.79	0.05		PHENOL HYDROXYLASE; CHAIN: A, B, C, D;	FLAVOPROTEIN, FAD, NADP FLAVIN FLAVIN, PHENOL HYDROXYLASE MONOOXYGENASE, OXIDOREDUCTASE
1680	1fum	A	12	43	3.2e-06	-0.74	0.37		FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A, M; FUMARATE REDUCTASE IRON-SULFUR PROTEIN; CHAIN: B, N; FUMARATE REDUCTASE 15 KD HYDROPHOBIC PROTEIN; CHAIN: C, O; FUMARATE REDUCTASE 13 KD HYDROPHOBIC PROTEIN; CHAIN: D, P;	OXIDOREDUCTASE COMPLEX II; COMPLEX II; COMPLEX II; COMPLEX II; FUMARATE REDUCTASE, COMPLEX II, SUCCINATE DEHYDROGENASE, 2 RESPIRATION, OXIDOREDUCTASE
1680	1fum	A	310	391	0.00032	-0.56	0.05		FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A, M; FUMARATE REDUCTASE IRON-SULFUR PROTEIN; CHAIN: B, N; FUMARATE REDUCTASE 15 KD HYDROPHOBIC PROTEIN; CHAIN: C, O; FUMARATE REDUCTASE 13 KD HYDROPHOBIC PROTEIN; CHAIN: D, P;	OXIDOREDUCTASE COMPLEX II; COMPLEX II; COMPLEX II; COMPLEX II; FUMARATE REDUCTASE, COMPLEX II, SUCCINATE DEHYDROGENASE, 2 RESPIRATION, OXIDOREDUCTASE
1680	1lpf	A	8	462	3.2e-95	-0.25	0.15		OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) COMPLEX WITH 1LPP 3 FLAVIN-ADENINE- DINUCLEOTIDE (FAD) 1LPP 4	
1680	1lvd		13	462	3.2e-75	-0.14	0.04		OXIDOREDUCTASE	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) COMPLEX WITH ILVL 3 NICOTINAMIDE-ADENINE-DINUCLEOTIDE (NAD <sup>+</sup> ) ILVL 4	
1680	1hhp		12	418	1.6e-57			76.88	OXIDOREDUCTASE (H2O2(A)) NADH PEROXIDASE (NPH) (E.C.1.1.1.1) MUTANT WITH CYS 42 INHP 3 REPLACED BY ALA (C42A) INHP 4	
1680	1oft		6	463	6.4e-88	-0.06	0.22		SURFACE PROTEIN; CHAIN: NULL;	OXIDOREDUCTASE REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE, NAD, 2 FLAVOPROTEIN, FAD, P64K
1680	1pyc	A	145	177	0.0048	0.02	0.11		L-ALANINE DEHYDROGENASE; CHAIN: A;	OXIDOREDUCTASE
1680	1qo8	A	4	49	6.4e-05	-0.43	0.06		FLAVOCTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A; D;	OXIDOREDUCTASE, NAD OXIDOREDUCTASE
1680	3lad	A	8	462	3.2e-91	-0.06	0.35		OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 31AD 3	
1681	1erj	A	173	479	1.6e-61	0.25	0.01		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1681	1erj	A	304	624	3.2e-72	0.56	0.99		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1681	1got	B	155	476	1.4e-55	0.43	-0.14		GT-ALPHA/GI-ALPHA GT-CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: G;	GAMMA1, TRANSUDIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1681	1got	B	179	524	1.4e-55			74.60	GT-ALPHA/AGI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSUDIN BETA SUBUNIT; GAMMA1, TRANSUDIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1681	1got	B	302	621	3.2e-74	0.76	0.71		GT-ALPHA/AGI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSUDIN BETA SUBUNIT; GAMMA1, TRANSUDIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1685	1osm	A	5	79	4.5e-10	0.86	-0.20		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANS MEMBRANE
1685	1osm	A	8	81	1.5e-12	1.11	-0.18		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANS MEMBRANE
1685	1pho		4	80	1.2e-11	0.90	-0.20		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE), IIPHIO 3	



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PstBlast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1685	2omf		8	80	1.3e-10	1.14	-0.19		MATRIX PORIN OUTER MEMBRANE PROTEIN F; ZOMF 5 CHAIN: NUL L; ZOMF 6	INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; ZOMF 7 PORIN, MEMBRANE PROTEIN ZOMF 12
1688	1eun	A	98	210	0.00015	-0.05	0.04		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2,2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1690	1ctt		14	124	9.6e-27	-0.02	0.22		HYDROLASE CYTIDINE DEAMINASE (CDA) (E.C.3.5.4.5) COMPLEXED WITH 1 ICTT 3,4-DIHYDROZEBULARINE (DHZ) ICTT 4	
1692	1a6d	A	15	186	8e-55	-0.12	1.00		THERMOSOME; CHAIN: A, B;	CHAPERONIN THERMOPLASMA ACIDOPHILUM, GROUP II CHAPERONIN, CCT, TRIC, 2 PROTEIN FOLDING, ATPASE
1692	1a6d	B	20	186	6.4e-51	-0.29	1.00		THERMOSOME; CHAIN: A, B;	CHAPERONIN THERMOPLASMA ACIDOPHILUM, GROUP II CHAPERONIN, CCT, TRIC, 2 PROTEIN FOLDING, ATPASE
1692	1der	A	12	186	1.6e-68	-0.14	0.72		GROEL; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N;	CHAPERONIN HSP60 CLASS, ATP, MAGNESIUM, CHAPERONIN
1692	1pht	A	5	106	0.00008	-0.18	0.23		PYRUVATE KINASE; CHAIN: A, B, C, D, E, F, H, G;	TRANSFERASE PYRUVATE KINASE, GLYCOLYTIC ENZYME, HOMOTETRAMER, 2 TRANSFERASE
1696	1alh	A	33	114	1.4e-09	0.06	-0.19		QSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING

SFQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1696	1alh	A	90	168	6.4e-27	0.07	-0.14		SITE; CHAIN: B, G; QKSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	PROTEIN COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1696	1mey	C	31	114	3.2e-19	0.07	-0.18		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1696	1mey	C	61	142	8e-35	0.10	-0.17		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1696	1mey	G	87	114	1.1e-09	0.16	-0.12		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1696	1h3	A	69	138	1.4e-13	0.08	-0.19		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIID; 5S GENE; NMR, TFIID, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1696	1ubd	C	63	168	3.2e-28	0.04	-0.14		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T A A	END A A	Fa Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1696	2gli	A	7	144	4.8e-17	0.03	-0.11		ZINC-FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	(TRANSCRIPTION REGULATORY DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1; ZINC-FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1698	1a9n	A	18	115	6.4e-13	0.03	0.94		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A; CHAIN: A; C; U2 B; CHAIN: B; D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNNP RIBONUCLEOPROTEIN
1698	1a9n	A	43	140	6e-11	-0.34	0.00		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A; CHAIN: A; C; U2 B; CHAIN: B; D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNNP RIBONUCLEOPROTEIN
1698	1a9n	C	18	115	6.4e-13	0.29	0.96		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A; CHAIN: A; C; U2 B; CHAIN: B; D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNNP RIBONUCLEOPROTEIN
1698	1a0b	A	18	140	1.4e-28	0.51	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1698	1a0c	A	14	114	3.2e-15	0.68	1.00		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A; C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B; D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1698	1a0c	A	39	137	3.2e-17	0.22	1.00		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A; C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B; D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT





SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1700	1evj	F	128	216	4.8e-25	0.46	0.64		O, P, Q, R, S, T; POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* O, P, Q, R, S, T; GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1700	1evj	H	128	233	6.4e-26	0.27	0.07		O, P, Q, R, S, T; POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* O, P, Q, R, S, T; GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1700	1evj	H	331	461	3e-21	0.72	1.00		O, P, Q, R, S, T; POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* O, P, Q, R, S, T; GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1700	1d8z	A	126	208	3.2e-22	0.30	0.71		HU ANTIGEN C; CHAIN: A; RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1700	1d8z	A	327	409	1.6e-17	0.93	0.83		HU ANTIGEN C; CHAIN: A; RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1700	1d9a	A	127	209	3.2e-16	0.55	0.00		HU ANTIGEN C; CHAIN: A; RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1700	1fnt	A	323	417	3e-17	0.71	0.58		UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL; NUCLEOLIN RBD2; CHAIN: A; RIBONUCLEOPROTEIN U1A17; RIBONUCLEOPROTEIN, RNP DOMAIN, SPICEOSOME	RIBONUCLEOPROTEIN U1A17; RIBONUCLEOPROTEIN, RNP DOMAIN, SPICEOSOME
1700	1fjc	A	321	412	1.5e-16	0.82	0.37		NUCLEOLIN RBD2; CHAIN: A; HNRNP A1; CHAIN: NULL; NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1,	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1700	1hal		126	301	4.8e-31	0.26	-0.17		HNRNP A1; CHAIN: NULL; NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1,	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1700	1ha1		226	405	1.6e-20	0.17	-0.19		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN, HNRNP, RED, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1700	1ha1		325	481	1.4e-34	0.78	0.99		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RED, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1700	1hd1	A	127	206	4.8e-23	0.82	0.77		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RED, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1700	1hd1	A	331	399	1.3e-20	0.86	0.98		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1700	lnc	A	127	209	1.6e-12	-0.09	0.49		RIBONUCLEOPROTEIN PROTEIN FROM UI SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP U1) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1-95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1700	lnc	B	127	207	1.3e-12	-0.19	0.43		RIBONUCLEOPROTEIN PROTEIN FROM UI SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									U1 INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	
1700	1qut9	A	128	217	4.8e-09	0.25	-0.14		POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN P7B, P7B-198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPLICING, 2 TRANSLATION
1700	1sxl		126	211	1.4e-15	0.06	0.33		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN) ISXL 3 (RBD-2), RESIDUES 199-294 PLUS N-TERMINAL MET) ISXL 4 (NMR, 17 STRUCTURES) ISXL 5	
1700	1urn	A	323	406	6e-16	0.71	0.99		U1A SPliceosomal PROTEIN; TURN 5 CHAIN: A, B, C; TURN 6 RNA 21MER HAIRPIN (5'-(AP*AP*UP*CP*AP*UP*UP*TURN 11 CHAIN: P, Q, R TURN 13	COMPLEX (RIBONUCLEOPROTEIN/RNA)
1700	2msl	A	127	206	3.2e-18	0.59	0.10		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1700	2sxl		126	210	1.3e-20	0.47	0.11		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1700	2sxl		328	411	1.1e-17	0.82	0.84		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1700	2ala		322	406	4.5e-16	0.60	0.96		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A;	NUCLEAR PROTEIN U1 SNRNP A PROTEIN; RNA BINDING DOMAIN;



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PAIF score	SEQFOLD score	Compound	PDB annotation
1700	2a2f	A	127	206	9.6e-13	0.53	0.05		CHAIN: NULL; SPLICING FACTOR, U2AF 65 KD SUBUNIT; CHAIN: A;	NUCLEAR PROTEIN RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN
1700	2up1	A	126	311	1.1e-34	0.01	-0.19		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRP A1; UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1700	2up1	A	226	410	4.8e-22	0.35	-0.14		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRP A1; UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1700	2up1	A	325	484	1.3e-35	0.49	0.87		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRP A1; UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1700	3sxl	A	329	474	3.2e-29	1.01	1.00		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 TERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1701	1a5c		35	191	4.5e-30			67.76	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1701	1awc	B	145	298	3e-45	0.92	1.00		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pd Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION) REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1701	lawc	B	150	298	1.1e-40	0.94	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION) REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION) REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1701	lawc	B	15	165	3e-39	0.90	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION) REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION) REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1701	lawc	B	17	165	1.6e-37	1.11	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION) REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION) REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1701	lawc	B	212	363	3e-45			90.41	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	COMPLEX (TRANSCRIPTION) REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
									DNA; CHAIN: D, E;	(TRANSCRIPTION REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1701	lawc	B	212	395	1.2e-41	0.64	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1701	lawc	B	250	427	3.2e-32	0.25	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1701	lawc	B	278	405	1e-32	1.07	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1701	lawc	B	45	199	6e-39	0.46	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1701	1awc	B	50	199	4.8e-37	0.72	1.00		GA BINDING PROTEIN ALPHA-CHAIN; A: GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATON/DNA) GARPALPHA; GARPETA I; COMPLEX (TRANSCRIPTION REGULATON/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1701	1bd8		113	299	3e-37	0.42	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1701	1bd8		145	301	1.4e-38			87.58	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1701	1bd8		17	168	7.5e-38	0.85	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1701	1bd8		183	333	1.5e-37	0.81	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1701	1bd8		215	397	1.4e-38	0.39	0.77		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1701	1bd8		279	405	4.5e-30	0.67	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1701	1bd8		46	201	1.4e-36	0.44	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1701	1bd8		82	234	1.4e-38	0.80	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1701	1bk	B	114	271	9e-38	0.72	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	ANKYRIN MOTIF COMPLEX (INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1701	1bk	B	12	170	1.5e-39			80.38	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1701	1bk	B	13	170	1.5e-39	0.92	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1701	1bk	B	183	338	1.4e-38	0.48	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1701	1bk	B	215	401	3e-39	0.43	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1701	1bk	B	46	205	9e-38	0.32	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										KINASE, CELL CYCLE 2 CONTROL, ALPHABETA COMPLEX (INHIBITOR PROTEIN/KINASE)
1701	1bu9	A	253	432	3.2e-30	0.24	0.25		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1701	1bu9	A	9	177	1.3e-35			92.05	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1701	1d98	A	104	237	3e-37	0.60	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1701	1d98	A	269	401	1.5e-36	0.80	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1701	1lib	A	253	431	1.4e-29	0.43	0.93		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1701	1lib	A	81	236	9e-38			80.22	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1701	1lic	D	145	371	1.2e-53	0.19	0.35		NE-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKCNFKB COMPLEX
1701	1lik	D	17	173	1.5e-39	0.71	1.00		NE-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKCNFKB COMPLEX

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1701	1lkn	D	212	427	1.1e-38	0.05	0.92		B-ALPHA; CHAIN: D; NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1701	1lkn	D	215	403	3e-50	0.49	0.99		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1701	1lkn	D	45	232	4.8e-43	0.11	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1701	1lkn	D	45	240	4.5e-52	0.13	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1701	1lkn	D	45	253	4.5e-52		81.35		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1701	1lkn	D	82	276	4.5e-52	0.28	0.99		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1701	1myo		247	391	1.5e-30	0.26	0.71		MYOTROPIN; CHAIN: NULL	ANK-REPEAT MYOTROPIN, ACETYLATION; NMR, ANK-REPEAT
1701	1inf	E	113	311	9e-51	0.58	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1701	1inf	E	143	401	3e-49	0.10	0.99		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									L-KAPPA-B-ALPHA; CHAIN: E; F;	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1701	1nfi	E	17	170	4.5e-39	0.94	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; L-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1701	1nfi	E	210	427	1.1e-38	0.42	0.70		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; L-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1701	1nfi	E	42	242	1.5e-51			87.55	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; L-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1701	1nfi	E	43	238	1.5e-51	0.50	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; L-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1701	1nfi	E	44	232	6.4e-43	0.59	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; L-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1701	1sw6	A	61	257	4.5e-36	-0.06	0.28		REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
1701	1sw6	A	76	320	4.5e-36			70.20	REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Ψi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1701	1yes	B	214	396	7.5e-35			70.78	P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENB 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1701	1yes	B	81	283	4.5e-37	-0.07	0.55		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENB 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1702	1a06		31	303	1.6e-70	0.08	0.65		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1702	1apm	E	29	312	6.4e-98	0.30	0.86		TRANSFERASE (PHOSPHOTRANSFERASE) SC-AMP <sup>+</sup> -DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (SC/APKS) IAPM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 IAPM 4 REPLACED BY ALA (S139A5) COMPLEX WITH THE PEPTIDE IAPM 5 INHIBITOR FQJ(5-24) AND THE DETERGENT MEGA-8 IAPM 6	
1702	1aq1		29	266	1.1e-46	0.22	0.11		CYCLIN-DEPENDENT PROTEIN	PROTEIN KINASE CDK2; PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	1st Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									KINASE 2; CHAIN: NULL;	KINASE, CELL CYCLE, PHOSPHORYLATION, STAUFORSPINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1702	1b3u	A	231	416	0.0003	0.22	1.00		PROTEINPHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A
1702	1b3u	A	278	560	1.4e-33	0.29	1.00		PROTEINPHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A
1702	1cmk	E	29	312	3.2e-99	0.10	0.75		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	PHOSPHORYLATION, HEAT REPEAT
1702	1ctp	E	29	303	8e-94	0.01	0.86		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	PHOSPHORYLATION, HEAT REPEAT
1702	1i3m	C	29	264	3.2e-49	0.35	0.98		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
1702	1hel		29	266	4.8e-49	0.26	0.60		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1702	1iia	A	328	551	6e-05	0.26	0.24		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1702	1koa		29	304	1.3e-58	0.30	0.75			ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1702	1kob	A	29	265	8e-57	0.51	0.96		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1702	1p38		3	334	3.2e-42			81.88	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
									MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1702	1pbk		31	264	6.4e-71	0.48	0.99		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1702	1vrk	A	301	453	1.1e-19	-0.18	0.09		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX/CALCIUM-BINDING PROTEIN/PEPTIDE
1702	2bct		438	560	0.0001	-0.31	0.52		BETA-CATENIN; CHAIN: NULL;	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-CATENIN, STRUCTURAL PROTEIN
1704	1lku		308	440	0.0003	-0.04	0.07		RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
1705	1bu2	A	157	352	3.2e-26	-0.26	0.30		CYCLIN HOMOLOG; CHAIN: A;	CELL CYCLE REGULATION CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL



SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1708	1got	B	242	569	1.6e-69			104.96	GT-ALPHA/ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	SIGNAL TRANSDUCTION COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT, GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1708	1got	B	280	569	1.6e-69	0.55	1.00		GT-ALPHA/ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT, GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1709	1a09	A	282	380	8e-25	0.56	0.09		C-SRC TYROSINE KINASE; CHAIN: A; B: ACE-FORMYL PHOSPHOTYR-GLU-Q-N-DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
1709	1ab2		282	382	1.6e-22	0.38	0.12		TRANSFERASE/PHOSPHOTRANSFERASE) PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.12) IAB2 3 (SRC HOMOLOG 2 DOMAIN) (ABELSON, SH2 ABL) IAB2 4 (NMR, 2D STRUCTURES) IAB2 5	
1709	1a0t	F	282	378	4.8e-21	0.47	0.06		FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN) SRC HOMOLOG 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1709	1bk1		284	385	1.6e-24	0.29	0.01		P660 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)
1709	1blj		275	379	1.6e-22	0.31	0.07		P55 BLK PROTEIN TYROSINE KINASE; CHAIN: NULL;	V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN; PHOSPHOTYROSINE RECOGNITION DOMAIN; P660/2 SRC SH2 DOMAIN PHOSPHORYLATION SIGNAL TRANSDUCTION, TYROSINE KINASE, TRANSFERASE, 2 PHOSPHOTRANSFERASE, PHOSPHORYLATION
1709	1csy	A	281	379	1.1e-17	0.44	-0.01		SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL-THR-PTA-GLU-THR-LEU-NH2; CHAIN: B;	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN; COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE)
1709	1ewd	L	286	375	1.4e-19	0.13	0.07		P56 LCK TYROSINE KINASE; CHAIN: L; PHOSPHONOPETIDE CHAIN: P;	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PHOSPHOTRANSFERASE, COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1709	1fhs		281	377	1.1e-17	0.18	0.15		GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	SH2 DOMAIN GRB2; GRB2, SH2 DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES
1709	1lek	A	242	379	6.4e-26	0.08	0.01		P56 LCK= TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGGPHOSPHOYQ92A; ILCK 14 CHAIN: B; ILCK 15	COMPLEX (KINASE/PEPTIDE)
1709	1lkk	A	282	379	3.2e-21	0.49	0.15		HUMAN P56 TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-ILE; ILCK 11 CHAIN: B; ILCK	COMPLEX (TYROSINE KINASE/PEPTIDE)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1709	1sha	A	284	380	1.6e-24	0.51	0.07	12	PHOSPHOTRANSFERASE V- SRC TYROSINE KINASE TRANSFORMING PROTEIN (PHOSPHOTYROSINE ISHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.112) COMPLEX WITH ISHA 4 PHOSHOPEPTIDE A (TYR-VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) ISHA 5	
1709	2pna		286	383	6.4e-18	0.33	0.78		SIGNALLING PROTEIN PHOSPHATIDYLINOSITOL 3- KINASE (E.C.2.7.1.137) (N- TERMINAL 2PNA 3 SH2 DOMAIN OF P85-ALPHA SUBUNIT) (NMR, 22 STRUCTURES) 2PNA 4 SHIP-2; CHAIN: A, B;	
1709	2shp	A	257	439	3.2e-27	-0.31	0.04		SHIP-2; CHAIN: A, B;	TYROSINE PHOSPHATASE SYP, SHIP-2; TYROSINE PHOSPHATASE, INSULIN SIGNALING, SH2 PROTEIN TRANSFERASE HCK, SH2, TYROSINE KINASE, SIGNAL TRANSDUCTION, TRANSFERASE
1709	3hck		281	379	1.6e-22	0.19	0.25		HCK SH2; CHAIN: NULL;	
1710	1a88	A	76	357	3e-41			85.13	CHLOROPEROXIDASE L; CHAIN: A, B, C;	HALOPEROXIDASE BROMOPEROXIDASE L, HALOPEROXIDASE L, HALOPEROXIDASE, OXIDOREDUCTASE
1710	1a88	A	84	356	3e-41	0.36	1.00		CHLOROPEROXIDASE L; CHAIN: A, B, C;	HALOPEROXIDASE BROMOPEROXIDASE L, HALOPEROXIDASE L, HALOPEROXIDASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1710	1a8q		78	360	8e-31			95.47	BROMOPEROXIDASE A1; CHAIN: NULL;	OXIDOREDUCTASE HALOPEROXIDASE CHLOROPEROXIDASE A1; HALOPEROXIDASE A1; HALOPEROXIDASE; OXIDOREDUCTASE
1710	1a8s		78	357	9e-41			83.84	CHLOROPEROXIDASE F; CHAIN: NULL;	HALOPEROXIDASE HALOPEROXIDASE F; HALOPEROXIDASE; OXIDOREDUCTASE, PROPIONATE COMPLEX
1710	1a8s		84	356	9e-41	0.61	1.00		CHLOROPEROXIDASE F; CHAIN: NULL;	HALOPEROXIDASE HALOPEROXIDASE F; HALOPEROXIDASE; OXIDOREDUCTASE, PROPIONATE COMPLEX
1710	1azw	A	63	355	1.5e-36			67.83	PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
1710	1b6g		44	357	3e-43			94.11	HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1710	1b6g		83	356	3e-43	0.45	1.00		HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1710	1brt		76	357	8e-32			89.86	BROMOPEROXIDASE A2; CHAIN: NULL;	HALOPEROXIDASE HALOPEROXIDASE A2; CHLOROPEROXIDASE A2; HALOPEROXIDASE, OXIDOREDUCTASE, PEROXIDASE, ALPHA/BETA 2 HYDROLASE FOLD, MUTANT M99T



SEQ ID NO:	PDB ID	CHAIN ID	STAR I AA	END AA	Pq Blast	Verity score	PMF score	SEQOL D score	Compound	PDB annotation
1710	1dx	A	72	357	3.2e-36			77.34	2-HYDROXY-6-OXO-6-PHENYLHEXA-2,4-DIENOATE CHAIN: A;	HYDROLASE BPHD; HYDROLASE, PCB DEGRADATION
1710	1eqw	A	67	360	9e-47			122.01	HALOALKANE DEHALOGENASE; 1-CHLOROHEXANE CHAIN: A;	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND
1710	1eqw	A	74	358	9e-47	0.58	1.00		HALOALKANE DEHALOGENASE; 1-CHLOROHEXANE CHAIN: A;	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND
1710	1ev2	A	73	358	3e-44	0.60	1.00		HALOALKANE DEHALOGENASE; CHAIN: A;	HYDROLASE LIND, 1,3,4,6-TETRACHLORO-1,4-CYCLOHEXADIENE DEHALOGENASE, LINDANE, BIODEGRADATION, ALPHA/BETA-HYDROLASE
1710	1ev1		101	199	3e-13	0.11	0.63		TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE TRIACYLGLYCEROL-HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE
1710	1ev1		97	212	4.8e-09	0.25	0.07		TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE TRIACYLGLYCEROL-HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE
1710	1ehy	A	66	356	9.6e-37			119.90	SOLUBLE EPOXIDE HYDROLASE; CHAIN: A, B, C, D;	HYDROLASE HYDROLASE, ALPHA/BETA HYDROLASE FOLD, EPOXIDE DEGRADATION, 2 EPICHLOROHYDRIN
1710	1ek1	A	62	356	8e-43	0.52	1.00		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR

SEQ NO:	PDB ID	CHAI ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1710	1ek1	A	70	356	1.2e-54	0.56	1.00		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1710	1ek1	B	62	356	8e-43	0.38	1.00		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1710	1ek1	B	69	356	3e-56	0.69	1.00		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, DISUBSTITUTED UREA 2 INHIBITOR
1710	1b1g	A	86	226	1.5e-06	0.13	0.07		LIPASE, GASTRIC; CHAIN: A, B;	HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE
1710	1qe3	A	85	215	4.5e-05	0.76	0.27		PARA-NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE DIRECTED EVOLUTION
1710	1qge	D	92	238	6e-25	0.38	0.81		TRIACYLGLYCEROL HYDROLASE; CHAIN: D; TRIACYLGLYCEROL HYDROLASE; CHAIN: E;	HYDROLASE PSEUDOMONADACEAE, CIS-PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID
1710	1qge	D	97	212	4.8e-09	0.37	0.28		TRIACYLGLYCEROL HYDROLASE; CHAIN: D; TRIACYLGLYCEROL HYDROLASE; CHAIN: E;	HYDROLASE PSEUDOMONADACEAE, CIS-PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID
1710	1qo7	A	74	358	1.5e-43	0.46	1.00		EPOXIDE HYDROLASE; CHAIN: A, B;	EPOXIDE HYDROLASE EH; EPOXIDE HYDROLASE; ALPHA/BETA HYDROLASE
1710	1qir	A	67	360	6.4e-29			80.11	PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA HYDROLASE FOLD; PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIN, AMINOPEPTIDASE
1710	4lip	D	97	215	4.8e-10	0.10	0.11		TRIACYLGLYCEROL-HYDROLASE; CHAIN: D, E;	LIPASE LIPASE; LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										ANALOGUE, ENANTIOSELECTIVITY
1711	1ehc		275	328	6e-17	-0.31	0.84		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1711	1ehc		278	332	3.2e-14	-0.18	0.71		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1711	1g25	A	276	321	4.5e-14	-0.64	0.00		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
1711	1rmd		272	328	3e-11	-0.02	0.74		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN VDJ RECOMBINATION ACTIVATING PROTEIN 1; RAG1, VDJ RECOMBINATION, ANTIBODY, MAD; RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1711	1rmd		280	331	1.3e-07	-0.00	0.64		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN VDJ RECOMBINATION ACTIVATING PROTEIN 1; RAG1, VDJ RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1712	1erz	A	194	297	0.009	0.16	0.12		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1712	1etj	A	171	307	1.4e-28	0.52	0.88		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1712	1ejj	A	37	289	1.3e-44	0.33	0.96		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A; B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1712	1got	B	14	290	6.4e-39	0.43	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: E; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1712	1got	B	1	307	1.6e-48			63.92	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1712	1got	B	58	305	1.6e-48	0.54	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1713	1dus	A	338	446	6.4e-10	-0.10	0.43		M0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
1713	1vid		334	455	7.5e-11	-0.07	0.30		CATECHOL O-METHYLTRANSFERASE; CHAIN: NULL;	TRANSFERASE (METHYLTRANSFERASE) COMET; TRANSFERASE.

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										METHYLTRANSFERASE, NEUROTRANSMITTER DEGRADATION
1719	1c46	A	345	497	3.2e-13	0.14	0.53		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2
1719	1c46	A	371	494	4.5e-16	0.50	0.96		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	HYPERHETEROSTABLE PROTEIN REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2
1719	1c41	A	20	170	0.0006	0.42	0.77		PROTEASE/HELICASE NS3; CHAIN: A, B;	HYPERHETEROSTABLE PROTEIN HYDROLASE HEPATITIS C VIRUS, BIFUNCTIONAL, PROTEASE-HELICASE
1719	1d2m	A	345	497	3.2e-13	0.09	0.52		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1719	1d2m	A	370	513	1.5e-16	-0.11	0.86		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1719	1d9x	A	346	525	3e-20	0.35	0.99		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1719	1d9x	A	354	508	3.2e-18	0.20	0.43		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1719	1fuk	A	338	508	1.1e-39	0.07	0.18		EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN
1719	1flu	A	2	169	1.6e-25	0.02	0.35		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A, EIF4A; HELICASE, DEAD-BOX PROTEIN
1719	1flu	B	119	508	0	0.04	-0.05		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A, EIF4A; HELICASE, DEAD-BOX PROTEIN
1719	1flu	B	2	169	1.6e-25	0.06	0.21		YEAST INITIATION FACTOR	TRANSLATION EUKARYOTIC

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1719	1hei	A	13	170	0.0014	0.29	0.22		4A; CHAIN: A, B;	INITIATION FACTOR 4A; IF4A; HELICASE, DEAD-BOX PROTEIN
1719	1qde	A	2	169	3.2e-23	0.10	0.39		HCV HELICASE; CHAIN: A, B;	HELICASE, DEAD-BOX PROTEIN
									TRANSLATION INITIATION FACTOR 4A; CHAIN: A;	HEPATITIS, HCV, ATPASE, NTPASE GENE REGULATION INITIATION, TRANSLATION INITIATION, SACCHAROMYCES CEREVISIAE, DEAD BOX 2 PROTEIN FAMILY
1719	2pjr	A	2	82	0.0006	0.22	0.33		HELICASE PCRA; CHAIN: A, F; HELICASE PCRA; CHAIN: B, G; DNA (5'-D*TP*TP*TP*TP*3'); CHAIN: C, D; DNA (5'-DC*GP*CP*3'); CHAIN: H; DNA (5'-D*AP*CP*TP*GP*CP*3'); CHAIN: I;	HYDROLASE/DNA ATP-DEPENDENT HELICASE PCRA; ATP-DEPENDENT HELICASE PCRA; HELICASE PCRA, HYDROLASE, DNA, PRODUCT COMPLEX
1721	1aox	A	28	170	1.1e-21	0.62	1.00		INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
1721	1aox	A	28	220	1.1e-21		75.90		INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
1721	1auz	A	31	213	4.8e-17		89.44		VON WILLEBRAND FACTOR; CHAIN: A, B;	COLLAGEN-BINDING COLLAGEN-BINDING, HEMOSTASIS, BINDING, HEMOSTASIS, DYNUCLEOTIDE BINDING FOLD
1721	1auq		23	221	1.6e-26		65.12		A1 DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	WILLERBRAND WILLERBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
1721	1auq		30	220	1.6e-26	0.79	0.99		A1 DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	WILLERBRAND WILLERBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
1721	1bpv		211	302	3.2e-11	0.22	-0.01		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1721	1bpv		329	427	9e-12	0.65	0.41		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN

SEQ ID NO:	PDB ID	CHAI ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1721	1bpv		342	418	3.2e-13	0.47	0.09		TTIN; CHAIN: NULL;	TYPE III CONNECTIN A71, CONNECTIN; TTIN, CONNECTIN, FIBRONECTIN TYPE III
1721	1bqv	A	337	419	3.2e-12	0.45	0.48		GF130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GPI30, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1721	1cfb		208	427	1.4e-11			52.60	NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	
1721	1cfb		209	412	1.4e-11	0.09	-0.07		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	
1721	1ck4	A	33	170	9.6e-21	0.46	1.00		INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN LDOMAIN, METAL BINDING, COLLAGEN, ADHESION
1721	1ck4	A	34	209	6e-38	0.96	1.00		INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN LDOMAIN, METAL BINDING, COLLAGEN, ADHESION
1721	1fna		338	415	1.1e-13	0.49	0.72		CELL ADHESION PROTEIN	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	FsI Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FIBRONECTIN CELL-ADHESION MODULE TYPE III-10, IFNA 3	
1721	1nf		106	444	1.4e-26	-0.05	0.13		FIBRONECTIN; IFN 6 CHAIN: NULL; IFN 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFN 18
1721	1nf		27	415	1.6e-31	-0.00	-0.06		FIBRONECTIN; IFN 6 CHAIN: NULL; IFN 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFN 18
1721	1nf		28	425	1.6e-31			91.50	FIBRONECTIN; IFN 6 CHAIN: NULL; IFN 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFN 18
1721	1fh	A	107	421	1.6e-24	0.16	-0.09		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1721	1fh	A	133	421	1.1e-26			73.33	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1721	1fh	A	213	445	1.1e-26	-0.04	0.49		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1721	1fh	A	30	217	1.6e-25	0.97	1.00		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
1721	1ido		32	208	7.5e-37			91.05	INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-ADHESION INTEGRIN, CELL GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX, CYTOSKELETON
1721	1ido		34	206	7.5e-37	0.65	1.00		INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-ADHESION INTEGRIN, CELL GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX, CYTOSKELETON
1721	1ifa	A	33	213	1.5e-36			76.17	CD11A; ILFA 3 CHAIN: A, B; ILFA 6	CELL ADHESION LFA-1, ALPHA-1A, BETA-2 INTEGRIN, A-DOMAIN;



SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1721	1lfn	A	34	209	1.5e-36	0.68	1.00		CD11A; ILFA 5 CHAIN: A, B; ILFA 6	ILFA 8 CELL ADHESION LFA-1 ALPHA- L BETA-2 INTEGRIN, A-DOMAIN; ILFA 8
1721	1mfn		211	425	6.4e-24			75.51	FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1721	1mfn		215	415	6.4e-24	0.08	0.38		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1721	1mfn		342	445	8e-17	0.42	0.37		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1721	1qc5	A	30	170	8e-21	0.55	1.00		ALPHA1 BETA1 INTEGRIN; CHAIN: A, ALPHA1 BETA1 INTEGRIN; CHAIN: B;	CELL ADHESION INTEGRIN, CELL ADHESION
1721	1qc5	A	34	209	7.5e-28	0.99	1.00		ALPHA1 BETA1 INTEGRIN; CHAIN: A, ALPHA1 BETA1 INTEGRIN; CHAIN: B;	CELL ADHESION INTEGRIN, CELL ADHESION
1721	1qg3	A	214	419	1.6e-18	0.05	-0.07		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1721	1qr4	A	214	421	1.6e-22	0.04	0.72		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T/AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1721	1qr4	A	214	421	1.6e-22			77.31	TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1721	1qr4	A	337	445	1.4e-13	0.55	0.34		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1721	1ten		210	301	3e-12	0.06	0.99		CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) ITEN 3	
1721	1ten		335	421	1.2e-13	0.92	0.81		CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) ITEN 3	
1721	1ttf		337	415	3.2e-14	0.27	0.70		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3 FIBRONECTIN; CHAIN: A;	
1721	2fmb	A	215	281	1.3e-06	0.55	0.84		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2
1721	2fmb	A	337	421	3.2e-11	0.71	0.86		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2
1721	2hft		215	416	1.1e-12	0.08	-0.17		HUMAN TISSUE FACTOR; 2HFT 4 CHAIN: NULL; 2HFT 5	COAGULATION FACTOR
1721	3lhr	B	215	422	1.5e-16	0.08	-0.19		HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsl Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4	
1723	1fhu	B	146	236	4.5e-06	0.19	0.58		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
1724	1a06		147	355	4.8e-39	-0.31	0.27		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1724	1apm	E	143	356	3.2e-47	-0.22	0.88		TRANSFERASE/PHOSPHOTRANSFERASE) 8C-AMPS-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (SC/APK5) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (S139AS) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PK(I3-24) AND THE DETERGENT MEGA-8 1APM 6	
1724	1apm	E	77	413	3.2e-47			59.46	TRANSFERASE/PHOSPHOTRANSFERASE) 8C-AMPS-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (SC/APK5) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (S139AS) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PK(I3-24) AND THE DETERGENT MEGA-8 1APM 6	
1724	1bi8	A	104	355	8e-24			52.92	CYCLIN-DEPENDENT KINASE	COMPLEX (KINASE/INHIBITOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									5; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1724	1cmk	E	143	356	1.6e-48	-0.22	0.70		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1724	1cmk	E	69	413	1.6e-48			59.27	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1724	1cnp	E	143	356	1.6e-48	-0.14	0.77		TRANSFERASE/PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATALYTIC SUBUNIT) ICTP 4	
1724	1cnp	E	77	399	1.6e-48			58.35	TRANSFERASE/PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATALYTIC SUBUNIT) ICTP 4	
1724	1f3m	C	147	361	4.8e-36	0.07	0.54		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
1724	1lan		77	401	1.1e-18			56.49	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1724	1kca		148	356	1.1e-33	-0.27	0.11		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1724	1kob	A	150	356	6.4e-34	-0.31	0.55		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1724	1p38		42	403	1.6e-24			60.82	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1724	1phk		127	356	3.2e-43	0.03	0.81		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1724	1pme		162	414	1.1e-24	-0.10	0.13		ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1724	1pme		83	392	1.1e-24			58.82	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1724	1tkl	A	150	362	3.2e-27	-0.27	0.54		TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1726	2hgs	A	3	66	0.0088	-0.23	0.52		GLUTATHIONE SYNTHETASE; CHAIN: A;	AMINE/CARBOXYLATE LIGASE
1728	1a9n	B	886	953	7.5e-07	0.40	0.52		U2 RNA HARPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B; CHAIN: B, D;	AMINE/CARBOXYLATE LIGASE
1728	1b7f	A	542	616	9e-05	0.26	0.95		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA(5'-	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRP, RIBONUCLEOPROTEIN RNA-BINDING PROTEIN/RNA TRA PRE-MRNA, SPLICING



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1728	1d9a	A	542	598	3e-05	0.48	0.80		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1728	1dm1	B	709	835	3e-06	-0.23	0.37		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1728	1fht		540	614	1.5e-05	0.65	0.68		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	RIBONUCLEOPROTEIN U1A17; RIBONUCLEOPROTEIN, RNP DOMAIN, SPLICOSOME
1728	1fj7	A	887	947	6e-07	0.48	0.21		NUCLEOLIN RBD1; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1728	1ha1		541	612	1.5e-05	0.42	0.99		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP; RNA BINDING, 2
1728	1hd1	A	560	614	6e-07	0.32	0.71		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D6; CHAIN: A;	RIBONUCLEOPROTEIN RNA-BINDING PROTEIN RNA-BINDING DOMAIN
1728	1hre	B	886	946	1e-08	0.13	0.99		RIBONUCLEOPROTEIN PROTEIN FROM U1 SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP U1) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	
1728	1qun9	A	493	614	7.5e-05	-0.14	0.22		POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB-C198; HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPLICING, 2 TRANSLATION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1728	1qm9	A	828	947	1.5e-07	0.10	0.10		POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTH, PTH-C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP; RNA, SPLICING, 2 TRANSLATION
1728	1xsl		540	610	0.0001	0.51	0.82		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN ISXL 3 (RBD-2), RESIDUES 199-294 PLUS N-TERMINAL MET) ISXL 4 (NMR, 17 STRUCTURES) ISXL 5	
1728	1urn	A	540	619	0.0001	-0.03	0.40		UIA SPLICOSOMAL PROTEIN; IURN 5 CHAIN: A, B, C; IURN 6 RNA 21MER HAREIN (5'-(AP*AP*UP*CP*AP*UP*UP* IURN 11 CHAIN: P, Q, R IURN 13	COMPLEX (RIBONUCLEOPROTEIN/RNA)
1728	2mss	A	560	614	1e-06	-0.03	0.03		MUSASHI; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1728	2xsl		542	614	4.5e-06	0.18	0.75		SEX-1LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1728	2ula		542	616	3e-05	0.42	0.39		UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	NUCLEAR PROTEIN UI SNRNP A; PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN
1728	2ula		887	946	6e-07	0.05	0.43		UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	NUCLEAR PROTEIN UI SNRNP A; PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN
1728	2up1	A	525	612	7.5e-07	0.51	0.75		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12 NUCLEOTIDE SINGLE-STRANDED	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1, COMPLEX (RIBONUCLEOPROTEIN/DNA)



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1728	2up1	A	889	947	7.5e-07	0.32	0.95		TELOMERIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
									HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMERIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1728	3sd	A	542	612	1e-05	0.58	1.00		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1728	3sd	A	889	958	3e-07	0.38	0.48		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1730	1e7f	A	199	336	0.0015	-0.27	0.17		SERUM ALBUMIN; CHAIN: A;	PLASMA PROTEIN PLASMA PROTEIN, METAL-BINDING, LIPID-BINDING
1733	1ahd	P	267	347	1.1e-28	-0.46	0.18		DNA-BINDING PROTEIN ANTENNAPEXIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 59 1AHD 3 REPLACED BY SER (C98) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1733	1b72	A	271	343	6.4e-24	-0.02	0.07	5	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA; CHAIN: D; DNA; CHAIN: E; DNA; CHAIN: F	PROTEIN/DNA HOMEOBOX, DNA COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1733	1b8f	A	270	340	6.4e-24	-0.12	0.46		ULTRABITHORAX HOMEOBOX PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEOBOX, HOMEOBOX PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1733	1fj1	A	266	341	3.2e-23	-0.04	0.92		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1733	1fj1	B	267	339	9.6e-22	0.38	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1733	11fb		271	336	6e-24	0.61	0.99		TRANSCRIPTION REGULATION TRANSCRIPTION FACTOR 1/FBI (HOMEOBOX) 1/FB 3	
1733	1pra		173	205	0.00015	0.08	0.51		GENE REGULATING PROTEIN REPRESSOR PROTEIN FROM BACTERIOPHAGE 434 (DNA-BINDING 1/PRA 3 DOMAIN, RESIDUES 1-69) (NMR, 20 STRUCTURES) 1/PRA 4	
1733	1m69		173	205	0.0003	0.15	0.78		GENE REGULATING PROTEIN REPRESSOR (AMINO-TERMINAL DOMAIN) (R1-69) 1/PRA 4	
1733	1san		273	347	1.6e-26	0.09	0.19		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEOBOX) MUTANT	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T-AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C398DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	
1733	1zuc		173	205	0.0003	-0.16	0.17		PHAGE 434 CRO PROTEIN; CHAIN: NULL;	TRANSCRIPTION REGULATION GENE REGULATING PROTEIN, TRANSCRIPTION REGULATION
1733	2ero		173	205	0.0003	-0.59	0.29		GENE REGULATING PROTEIN CRO PROTEIN 2CRO 4	
1733	9ant	A	271	341	3.2e-26	-0.27	0.04		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1734	1ahd	P	267	347	1.6e-28	-0.46	0.18		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C398) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1734	1b72	A	271	343	1.6e-24	-0.02	0.07		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E; DNA CHAIN: F; PROTEIN/DNA	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1734	1b8i	A	271	340	8e-24	-0.31	0.28		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN; CHAIN: B; EXTRAADENTICLE; CHAIN: B; DNA (5'-CHAIN: C; DNA (5'-CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1734	1fj1	A	266	341	1.6e-23	-0.04	0.92		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1734	1fil	B	267	339	8e-22	0.38	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1734	1lfb		271	336	6e-24	0.61	0.99		TRANSCRIPTION REGULATION TRANSCRIPTION FACTOR	
1734	1pra		173	205	0.00015	0.08	0.51		LFBI (HOMEODOMAIN) 1LFB, 3 GENE REGULATING PROTEIN FROM BACTERIOPHAGE 434 (DNA-BINDING 1PRA 3 DOMAIN, RESIDUES 1-69) (NMR, 20 STRUCTURES) 1PRA 4	
1734	1r69		173	205	0.0003	0.15	0.78		GENE REGULATING PROTEIN REPRESSOR (AMINO-TERMINAL DOMAIN) (R1-69) 1R69 4	
1734	1san		273	347	6.4e-26	0.09	0.19		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	
1734	1xag		173	205	0.0003	-0.16	0.17		PHAGE 434 CRO PROTEIN; CHAIN: NULL;	TRANSCRIPTION REGULATION GENE REGULATING PROTEIN, TRANSCRIPTION REGULATION
1734	2cro		173	205	0.0003	-0.59	0.29		GENE REGULATING PROTEIN CRO PROTEIN 2CRO 4	
1734	9ant	A	271	341	8e-26	-0.27	0.04		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD;

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									D, E, F;	HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1738	1aj4		1	101	4.8-30	-0.11	0.06		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1738	1aj4		23	170	1.4-38			82.97	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1738	1aj4		25	169	1.4-38	0.17	0.70		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1738	1ak8		30	104	1.1-29			75.36	CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERUM TRIC- DOMAIN, RESIDUES 1-75; CERUM- LOADED, CALCIUM-BINDING PROTEIN
1738	1ap4		22	109	6.4-23			61.36	CARDIAC N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING CTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, CARDIAC MUSCLE 2 CONTRACTION
1738	1ati	B	1	101	3.2-20	0.08	-0.01		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1738	1avs	A	26	106	3.2-26			70.90	TROPONIN C; CHAIN: A, B;	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN
1738	1blq		20	109	8-27			71.63	N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING, REGULATION, TROPONIN C, SKELETAL MUSCLE, 2 CONTRACTION
1738	1br1	B	33	170	4.8-34			57.30	MYOSIN; CHAIN: A, B, C, D, E;	MUSCLE PROTEIN MDE; MUSCLE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1738	1bu3		2	103	3.2e-11			50.72	F, G, H; CALCIUM-BINDING PROTEIN; CHAIN: NULL;	PROTEIN CALCIUM BINDING CALCIUM BINDING
1738	1cdm	A	1	102	8e-35	0.01	0.82		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
1738	1cdm	A	33	158	1.4e-47			85.63	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
1738	1cdm	A	33	169	1.4e-47	0.08	0.92		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
1738	1ell		1	102	3.2e-35	-0.09	0.40		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1738	1ell		33	169	9.6e-53	-0.02	0.81		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1738	1ell		33	170	9.6e-53			89.82	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1738	1cmf		33	104	7.5e-23			68.52	CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; ICMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; ICMF 9
1738	1dlt	A	1	101	4.8e-29	0.00	0.28		CARDIAC TROPONIN C;	STRUCTURAL PROTEIN HELIX-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Coumpound	PDB annotation
1738	1ddi	A	31	169	9.6e-36	0.26	0.72		CHAIN: A; CARDIAC TROPONIN C; CHAIN: A;	TURN-HELIX STRUCTURAL PROTEIN HELIX- TURN-HELIX
1738	1exr	A	1	101	3.2e-34	-0.11	0.80		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1738	1exr	A	31	169	4.8e-51	0.03	0.89		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1738	1pva	A	7	104	1.6e-15			55.26	CALCIUM BINDING PARVALBUMIN (PIKE, PI 5.0, ALPHA COMPONENT) COMPLEXED WITH 1PVA A 1 TWO CALCIUM IONS (SYNCHROTRON X-RAY DIFFRACTION) 1PVA A 2	
1738	1rtp	1	7	104	3.2e-16			55.44	CALCIUM-BINDING PROTEIN ALPHA-PARVALBUMIN (RTP 3 TROPONIN C; CHAIN: NULL;	
1738	1icf		1	101	1.1e-30	-0.10	0.35			CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION
1738	1icf		24	169	1.6e-41			89.65	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION
1738	1icf		33	169	1.6e-41	-0.13	0.96		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQBOL D score	Compound	PDB annotation
										CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1738	1lux		1	101	9.6e-34	-0.26	0.41		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND ITNX 14
1738	1lux		24	169	1.6e-38			84.53	TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND ITNX 14
1738	1lux		33	169	1.6e-38	0.17	0.94		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND ITNX 14
1738	1top		1	101	3.2e-32	-0.20	0.30		CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1738	1top		20	169	4.8e-42			86.96	CONTRACTILE SYSTEM	
1738	1top		33	169	4.8e-42	0.13	1.00		PROTEIN TROPONIN C ITOP 3	
1738	1trc	A	36	103	8e-22			62.97	CONTRACTILE SYSTEM CALCIUM BINDING PROTEIN CALMODULIN (TR-2-C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
1738	1trf		31	106	3.2e-26			66.58	MUSCLE PROTEIN TROPONIN C (TRIC FRAGMENT) (APO FORM) (NMR, 1 STRUCTURE) 1TRF 3	
1738	1trk	A	1	104	9.6e-36	-0.06	0.36		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1738	1trk	A	31	170	1.1e-51			90.09	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1738	1wk	A	33	169	1.1e-51	0.15	0.95		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1738	1wde	B	33	170	7.5e-26			64.97	SCALLOP MYOSIN; CHAIN: A; B; C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1738	1wde	C	33	171	1.1e-25			54.16	SCALLOP MYOSIN; CHAIN: A; B; C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1738	3cin		31	104	8e-10			32.43	TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CTNC; CARDIAC MUSCLE REGULATORY, CALCIUM-BINDING PROTEIN
1738	4cpv		6	103	1.3e-11			51.70	CALCIUM BINDING CALCIUM-BINDING PARVALBUMIN (3P*1=4,25) 4CPV 3	
1745	1ukz		362	463	0.0006	-0.05	0.07		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	
1745	1zak	A	362	587	0.0001	-0.17	0.13		ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE ATP-AMP-PHOSPHOTRANSFERASE, TRANSFERASE
1745	3adk		362	495	0.0075	-0.25	0.16		TRANSFERASE(PHOSPHOTRANSFERASE)ADENYLATE KINASE (E.C.2.7.4.5) 3ADK 4	
1746	1ukz		362	463	0.0006	-0.05	0.07		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1746	1zak	A	362	587	0.0001	-0.17	0.13		ADENYLATE KINASE, CHAIN: A, B;	TRANSFERASE ATP-AMP- PHOSPHOTRANSFERASE, TRANSFERASE
1746	3adk		362	495	0.0075	-0.25	0.16		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1749	1btk	A	53	142	6e-06	-0.50	0.04		BRUTON'S TYROSINE KINASE, CHAIN: A, B;	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK; TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2 AGAMMAGLOBULINEMIA, TYROSINE-PROTEIN KINASE
1749	1fao	A	55	142	3e-15	0.14	0.83		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1749	1fb8	A	48	142	3e-16	0.25	0.99		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1749	1fgv	A	52	142	7.5e-12	-0.02	0.75		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
1750	1sm1	A	3	178	1.6e-14	0.08	-0.14		PENICILLINASE, CHAIN: A;	HYDROLASE METALLO-BETA-LACTAMASE, ANTIBIOTIC RESISTANCE, BINUCLEAR 2 ZINC, HYDROLASE

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOI, D score	Compound	PDB annotation
1750	2bc2	A	3	170	1.6e-14	0.18	-0.05		METALLO BETA-LACTAMASE II; CHAIN: A, B;	HYDROLASE HYDROLASE, BETA-LACTAMASE, ANTIBIOTIC, METALLOENZYME
1751	1byc		1	711	0			253.58	LIPOXYGENASE-3; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, METALLOPROTEIN, FE(II) COMPLEX, CATECHOL
1751	1byc		35	711	0	0.36	1.00		LIPOXYGENASE-3; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, METALLOPROTEIN, FE(II) COMPLEX, CATECHOL
1751	1eal		7	111	1.6e-20	-0.01	0.04		ALPHA-TOXIN; CHAIN: NULL;	HYDROLASE PHOSPHOLIPASE C; ZINC PHOSPHOLIPASE C; GANGRENE DETERMINANT, C2 DOMAIN CA 2 AND MEMBRANE BINDING HYDROLASE
1751	1eth	A	4	99	0.0045	0.46	0.45		TRIACYLGLYCEROL ACYL-HYDROLASE; CHAIN: A, C; COLIPASE; CHAIN: B, D	COMPLEX (HYDROLASE/COFACTOR) TRIACYLGLYCEROL LIPASE; COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION
1751	1lox		2	711	0	0.41	1.00		15-LIPOXYGENASE; CHAIN: NULL;	OXIDOREDUCTASE 15-OX; OXIDOREDUCTASE 15LO DEPOT2
1751	1lox		2	711	0		482.93		15-LIPOXYGENASE; CHAIN: NULL;	OXIDOREDUCTASE 15LOX; OXIDOREDUCTASE 15LO DEPOT2
1751	1yge		1	711	0		231.83		LIPOXYGENASE-1; CHAIN: NULL;	DIOXYGENASE L-1; DIOXYGENASE, LIPOXYGENASE, METALLOPROTEIN, FATTY ACIDS
1751	1yge		46	711	0	0.18	1.00		LIPOXYGENASE-1; CHAIN: NULL;	DIOXYGENASE L-1; DIOXYGENASE, LIPOXYGENASE, METALLOPROTEIN, FATTY ACIDS

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsl Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1753	1cc0	E	24	162	4.5e-66	0.50	1.00		TRANSFORMING PROTEIN RHOA; CHAIN: A; C: RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G-PROTEIN, SIGNALING PROTEIN
1753	1cc0	E	24	177	9.6e-70	0.53	1.00		TRANSFORMING PROTEIN RHOA; CHAIN: A; C: RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G-PROTEIN, SIGNALING PROTEIN
1753	1doe	B	5	162	6e-76	0.48	1.00		GTP-BINDING PROTEIN; CHAIN: A; GDP-DISSOCIATION INHIBITOR 1; CHAIN: B;	CELL CYCLE CDC42; RHO GDI 1; GTP-BINDING PROTEIN, CDC42, RHOGDI, X-RAY
1753	1doe	B	5	180	1.6e-78	0.48	1.00		GTP-BINDING PROTEIN; CHAIN: A; GDP-DISSOCIATION INHIBITOR 1; CHAIN: B;	CELL CYCLE CDC42; RHO GDI 1; GTP-BINDING PROTEIN, CDC42, RHOGDI, X-RAY
1757	1ahd	P	19	86	6.4e-36			70.63	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1757	1ahd	P	20	85	6.4e-36	-0.12	0.90		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1757	1b72	A	21	81	3e-31	-0.15	0.98		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1757	1b72	A	24	81	3.2e-28	0.19	0.99		HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN; DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1757	1b72	A	9	81	3e-31			64.24	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN; DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1757	1b88	A	20	77	6.4e-31			64.34	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1757	1b88	A	2	78	6.4e-31	-0.14	0.82		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1757	1ftz		18	86	4.8e-32			66.44	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	
1757	1ftz		19	85	4.8e-32	-0.01	0.81		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	
1757	1oct	C	1	79	3e-31	-0.70	0.23		DNA-BINDING PROTEIN OCT-1 (POU DOMAIN) 1OCT 3	
1757	1san		25	86	1.5e-33			65.69	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S)DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	

SEQ NO;	PDB ID	CHAIN ID	STAR T AA	END AA	PSI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1757	1san		26	85	1.6e-33	-0.17	0.98		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C59S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	
1757	9ant	A	24	79	1.6e-33	-0.13	1.00		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1757	9ant	A	24	79	1.6e-33			68.97	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1758	1a3y	A	38	169	3e-35	0.63	0.86		ODORANT BINDING PROTEIN; CHAIN: A, B;	LIPOCALIN LIPOCALIN, OLFACTION
1758	1dfv	A	20	169	4.5e-47	0.66	1.00		HUMAN NEUTROPHIL GELATINASE; CHAIN: A, B;	SUGAR BINDING PROTEIN NGAL; NEUTROPHIL, NGAL, LIPOCALIN
1758	1ew3	A	30	169	1.4e-38	0.90	0.95		ALLERGEN EQU C 1; CHAIN: A;	ALLERGEN LIPOCALIN, BETA BARREL
1758	1mup		25	168	6e-37	0.78	1.00		PEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL) IMUP 3 THIAZOLINE IMUP 4	
1758	1mup		25	168	6e-37			64.35	PEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL) IMUP 3 THIAZOLINE IMUP 4	
1758	1obp	A	30	172	9e-36	0.19	-0.02		ODORANT-BINDING PROTEIN; CHAIN: A, B;	ODORANT-BINDING PROTEIN OBP OLFACTION, NOSE, TRANSPORT, LIPOCALIN, ODORANT-BINDING 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1758	1qps	A	17	169	4.5e-40	0.83	1.00		NEUTROPHIL GELATINASE; CHAIN: A;	PROTEIN
1758	1btp		26	168	1e-35	0.14	-0.09		RETINOL TRANSPORT RBP 3	SUGAR BINDING PROTEIN NGAL; NEUTROPHIL LIPOCALIN, SIGNAL PROTEIN, GLYCOPROTEIN
1758	2a2u	A	25	169	1.3e-36	0.69	0.99		ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	LIPID BINDING PROTEIN A2U-GLOBULIN, LIPID BINDING PROTEIN
1758	2a2u	A	25	169	1.5e-37	0.91	1.00		ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	LIPID BINDING PROTEIN A2U-GLOBULIN, LIPID BINDING PROTEIN
1758	2a2u	A	25	169	1.5e-37			78.30	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	LIPID BINDING PROTEIN A2U-GLOBULIN, LIPID BINDING PROTEIN
1759	1atv	H	21	249	1.6e-94	0.30	1.00		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB253 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB3 HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
1759	1ao7	E	22	263	4.8e-64			295.76	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1759	1aql	H	22	252	1.6e-95	0.48	1.00		FAB B7-15A2; CHAIN: L, H;	IMMUNOGLOBULIN HUMAN FAB, ANTI-TETANUS TOXOID, HIGH AFFINITY, CRYSTAL 2 PACKING MOTIF, PROGRAMMING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1759	1bd2	E	22	263	1.2e-98	0.74	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	PROPSINITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN
1759	1bd2	E	22	263	1.2e-98			386.70	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1759	1dbb	H	21	252	9.6e-94	0.30	1.00		IMMUNOGLOBULIN 3D6 FAB IDPB 3	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1759	1lvd	B	21	252	6.4e-96	0.41	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5; VERSION 4 IFVD 3	
1759	1hyx	H	21	252	4.8e-95	0.47	1.00		IMMUNOGLOBULIN 6D9; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB, 2 IMMUNOGLOBULIN
1759	1lge	H	22	252	1.6e-95	0.21	1.00		COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DONALD III) IGC: 5 PROTEIN G; STREPTOCOCCUS IGC 15	
1759	1lgt	B	21	263	8e-99	0.42	0.99		IGGA INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1759	1ngp	H	21	249	1.6e-93	0.35	1.00		NI69 (GGI-LAMBDA=); CHAIN: L, H;	REGION, IMMUNOGLOBULIN
1759	2hrp	H	22	251	3.2e-93	0.39	1.00		MONOCLONAL ANTIBODY FI12.32; CHAIN: L, H, M, N; HIV-1 PROTEASE PEPTIDE; CHAIN: P, Q;	IMMUNOGLOBULIN, IMMUNOGLOBULIN, COMPLEX (IMMUNOGLOBULIN/PEPTIDE) IMMUNOGLOBULIN, IGG1; FAB FRAGMENT, CROSS-REACTIVITY, HIV1 PROTEASE, ENZYME 2 INHIBITION, COMPLEX (IMMUNOGLOBULIN/PEPTIDE)
1762	1dan	L	64	195	6e-10			50.68	BLOOD COAGULATION FACTOR V1A; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U, D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX, SERINE PROTEASE/COFACTOR/LIGAND
1762	1ehd	A	12	88	1.1e-07	0.40	0.01		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1762	1eis	A	12	88	3e-08	0.06	-0.12		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPRANTIGEN
1762	1en2	A	12	88	6e-09	-0.20	0.00		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPRANTIGEN, SACCHARIDE BINDING
1762	1ext	A	37	192	3e-12			62.34	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
1762	1ext	A	57	203	3e-12	-0.34	0.36		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
1762	1fvl		31	101	1.2e-12	-0.37	0.04		FLAVORIN; IFVL 4 CHAIN;	BLOOD COAGULATION INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1762	1klo		15	184	4.5e-19	0.17	-0.12		NULL; IFVL 5	GP IIB/IIIA ANTAGONIST; IFVL 9
1762	1klo		48	203	1.3e-20			66.44	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1762	1ncf	A	17	140	7.5e-09	-0.24	0.23		LAMININ; CHAIN: NULL; TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A; B; INCF 5	GLYCOPROTEIN GLYCOPROTEIN SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19
1762	1ncf	A	55	189	7.5e-11			55.28	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A; B; INCF 5	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19
1762	1pfx	L	41	176	3e-14			57.36	FACTOR IXA; CHAIN: C, L; D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/ARG, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM/ BINDING, HYDROLASE, 3 GLYCOPROTEIN
1762	1skz		19	121	3e-17	0.05	0.15		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1762	1skz		57	161	1.5e-18			65.03	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1762	1skz		58	161	3e-18	-0.14	0.12		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1762	1skz		98	204	4.5e-17	0.13	-0.08		ANTISTASIN; CHAIN: NULL;	STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1762	1vmo	A	35	190	9e-33	0.36	-0.15		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I IVMO 3	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1762	2psp	A	90	191	0.0014			61.72	PORCINE PANCREATIC SPASMOLYTIC POLYPEPTIDE; CHAIN: A, B;	TREFOIL FAMILY OF PEPTIDES PSP REPEAT, GROWTH FACTOR, SIGNAL
1762	9wga	A	13	133	1.5e-18	0.12	0.13		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1762	9wga	A	32	191	6e-29			97.20	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1768	1bta		200	234	0.003	-0.02	0.70		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
1768	1byn	A	245	347	0.0043	0.52	0.24		SYNAPTOTAGMIN 1; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, NEUROTRANSMITTER 2 RELEASE, EXOCYTOSIS
1768	1byn	A	245	349	1.2e-11	0.04	0.01		SYNAPTOTAGMIN 1; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1768	1qpv	A	247	362	4.5e-05	0.47	0.54		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SANDWICH, CALCIUM ION, C2 DOMAIN
1768	1fao	A	173	235	6e-05	0.07	0.36		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1768	1fbs	A	173	239	9e-06	-0.29	0.70		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1768	1nfl	A	400	687	7.5e-68			108.36	NEUROFIBROMIN; CHAIN: A;	SIGNALING PROTEIN NFI-333; NEUROFIBROMIN, TYPE I NEUROFIBROMATOSIS, NFI, RAS, GAP, 2 SIGNAL TRANSDUCTION, CANCER, GROWTH REGULATION, GTP 3 HYDROLYSIS, PATIENT MUTATION, ARGININE FINGER
1768	1nfl	A	416	682	7.5e-68	0.21	0.99		NEUROFIBROMIN; CHAIN: A;	SIGNALING PROTEIN NFI-333; NEUROFIBROMIN, TYPE I NEUROFIBROMATOSIS, NFI, RAS, GAP, 2 SIGNAL TRANSDUCTION, CANCER, GROWTH REGULATION, GTP 3 HYDROLYSIS, PATIENT MUTATION, ARGININE FINGER
1768	1pls		173	239	4.5e-05	0.33	0.37		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOMOLOGY DOMAIN) MUTANT 1PLS 3	







SEQ NO:	PDB ID	CHAI ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1770	1ht		230	315	1.5e-11	0.37	0.12		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	BINDING DOMAIN RIBONUCLEOPROTEIN U1A117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPliceosome
1770	1fc	A	222	313	3.2e-12	0.30	0.07		NUCLEOLIN RB12; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C2; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1770	1ha1		129	314	4.8e-45	0.17	-0.09		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1770	1ha1		231	425	1.5e-40	0.21	0.95		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1770	1ha1		350	431	1.5e-16	0.83	0.94		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1770	1hd1	A	136	213	6.4e-20	0.03	-0.19		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1770	1hd1	A	237	314	4.8e-22	0.78	0.16		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1770	1hd1	A	351	425	9.6e-15	0.91	0.68		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN



SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1770	1qm9	A	238	427	4.8e-19	0.06	0.15		POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB-C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPLICING, 2 TRANSLATION
1770	1sxl		223	319	1.6e-18	0.21	-0.15		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN ISXL 3 (RBD-2), RESIDUES 199-294 PLUS N-TERMINAL MET) ISXL 4 (NMR, 17 STRUCTURES) ISXL 5	
1770	1sxl		341	429	3.2e-13	0.51	0.13		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN ISXL 3 (RBD-2), RESIDUES 199-294 PLUS N-TERMINAL MET) ISXL 4 (NMR, 17 STRUCTURES) ISXL 5	
1770	2mss	A	136	213	1.3e-14	0.11	-0.18		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1770	2mss	A	237	314	6.4e-19	0.74	0.17		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1770	2mss	A	351	425	4.8e-14	0.91	0.99		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1770	2sxl		236	322	1.1e-19	0.36	0.25		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1770	2sxl		348	431	4.8e-14	0.42	0.70		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1770	2a2f	A	256	314	6.4e-18	0.75	0.88		SPLICING FACTOR UZAF 65 KD	RNA-BINDING PROTEIN SPLICING,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
									SUBUNIT; CHAIN: A;	U2 SNRNP, RBD, RNA-BINDING PROTEIN
1770	2up1	A	128	319	4.8e-47	0.00	0.09		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UPI, COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1770	2up1	A	231	433	1.6e-43	0.60	0.52		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UPI, COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1770	3ss1	A	133	307	3.2e-36	0.22	-0.02		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1770	3ss1	A	236	425	1.4e-32	0.32	0.96		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1772	1alh	A	363	445	3.2e-31			74.27	QSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1772	1ney	C	138	219	9.6e-44	-0.22	0.04		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	166	247	4.8e-46	0.35	0.96		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	194	275	4.8e-47	0.14	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	222	303	1.3e-47	0.54	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	250	331	3.2e-48	0.24	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	278	359	1.1e-49	0.71	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	306	387	3.2e-50	0.74	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fs Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1772	1mey	C	334	415	1.6e-51	0.69	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	362	443	4.8e-51	-0.02	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	390	471	9.6e-51	0.37	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	418	499	1.6e-50	0.52	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	446	527	1.6e-50	0.31	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	446	528	1.6e-50			102.60	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	474	531	6.4e-34	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1772	1mey	G	164	191	9.6e-11	0.55	0.05		DNA; CHAIN: A, B, D, E; SENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	G	44	71	1.6e-09	-0.73	0.29		DNA; CHAIN: A, B, D, E; SENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1uf6	A	167	312	1.3e-35	0.24	0.54		TTT1A; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1772	1uf6	A	223	368	4.8e-37	0.28	0.96		TTT1A; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1772	1uf6	A	307	452	3.2e-38	0.07	0.99		TTT1A; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1772	1uf6	A	334	497	3.2e-38			100.49	TTT1A; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1772	1hf6	A	363	509	1.6e-37	-0.06	0.95		TTIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1772	1it6	A	391	529	1.4e-36	0.01	0.94		TTIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1772	1ubd	C	143	247	4.8e-32	0.07	0.11		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1772	1ubd	C	169	275	1.5e-23	-0.21	0.72		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T A A	END A A	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1772	1ubd	C	199	303	4.5-43	0.13	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1772	1ubd	C	202	303	1.6-32	0.02	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1772	1ubd	C	223	359	1.5-46	0.21	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1772	1ubd	C	258	359	4.8-34	0.36	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1772	1ubd	C	332	443	1.5-50	0.03	1.00		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1772	1ubd	C	360	472	6e-52	0.06	1.00		YY1; CHAIN: C; ADENOVIRUS ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1772	1ubd	C	388	499	9e-51	-0.01	0.90		YY1; CHAIN: C; ADENOVIRUS ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1772	1ubd	C	416	527	3e-50	0.01	1.00		YY1; CHAIN: C; ADENOVIRUS ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1772	1ubd	C	420	528	9e-51			82.44	YY1; CHAIN: C; ADENOVIRUS ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verity score	PMF score	SEQOL D score	Compound	PDB annotation
									CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1772	1ubd	C	426	527	8e-35	0.11	1.00		YY1; CHAIN: C; ADENOVIRUS P3 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1772	2adr		139	193	8e-14	0.11	-0.18		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1772	2gli	A	102	246	3.2e-29	-0.10	0.13		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	197	389	3e-58	0.26	0.95		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	278	417	9e-64	0.51	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	306	443	1.5e-63	0.21	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	362	501	1.5e-67	0.31	0.98		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END A A	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1772	2gli	A	362	501	1.5e-67			88.77	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	390	524	1.5e-49	-0.07	0.84		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	398	529	1.6e-34	0.24	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1774	1bor		10	59	4.8e-06	-0.87	0.07		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION
1774	1che		11	59	1.3e-11	-0.50	0.52		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC3 (NMR, 1 STRUCTURE) 1CHC4	PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
1774	1che		15	63	3.2e-06	-0.28	0.39		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC3 (NMR, 1 STRUCTURE) 1CHC4	
1774	1bvv	A	14	69	1.2e-12	0.41	0.41		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCHE7; CHAIN: C;	LIGASE CBL, UBCHE7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
1774	1bvv	A	15	59	3.2e-06	-0.34	0.21		SIGNAL TRANSDUCTION	LIGASE CBL, UBCHE7, ZAP-70, E2,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Ps Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 (DA UBCH7; CHAIN: C; NUCLEAR FACTOR XNF7; CHAIN: NULL;	UBIQUITIN E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
1774	1fre		93	128	1.5e-13	-0.23	0.36			ZINC-BINDING PROTEIN ZINC-BINDING PROTEIN, XNF7, BBOX, DEVELOPMENT, 3 MID-BLASTULA-TRANSITION
1774	1g25	A	11	70	4.5e-14	0.21	0.74		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
1774	1quu	A	63	304	3e-06			54.69	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1774	1rmd		11	100	4.5e-20	-0.03	0.84		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1774	1rmd		9	109	6.4e-14	-0.19	0.01		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1775	1um	A	248	414	4.5e-07	-0.07	0.19		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
										STRUCTURAL PROTEIN
1776	1cm	A	1	93	9e-10	0.34	-0.13		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2-TANDEM 3-HELIX COILED-COILS, ENDOCYTOSIS/EXOCYTOSIS
1776	1oz3	A	9	124	4.5e-09	0.10	-0.12		SYNTAXIN-1A; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C; SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1777	1abc		516	553	0.0006	0.21	0.18		VIRUS EQUINE HERPES VIRUS-1 (C3HC4 OR RING DOMAIN) ICHC 3 (NMR, 1 STRUCTURE) ICHC 4	
1780	1eo0	A	1	78	4.5e-06	-0.14	0.52		TRANSCRIPTION ELONGATION FACTOR S-II; CHAIN: A;	TRANSCRIPTION HELIX-BUNDLE
1780	1qpp		291	343	0.00045	-0.51	0.51		RNA POLYMERASE II; CHAIN: NUT1;	TRANSCRIPTION TRANSCRIPTION, RNA POLYMERASE II SUBUNIT, RPB9, ZN RIBBON, 2 HYPERTHERMOPHILIC, EXTREMOPHILE
1780	1hfi		286	345	1.6e-10	0.16	1.00		TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII (TFIS, NUCLEIC-ACID ITF1 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) ITF1 4	
1780	1hfi		287	343	4.5e-11	-0.07	0.75		TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
									(TFIIIS, NUCLEIC-ACID (TFII 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) (TFI 4	
1781	1aaj	A	458	510	1.5e-14	-0.85	0.01		EPS8; CHAIN: A, B;	SIGNAL TRANSDUCTION SRC HOMOLGY DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, EPS8, PROLINE RICH PEPTIDE
1781	1awj		436	507	3e-14	0.30	0.82		ITK; CHAIN: NULL;	TRANSFERASE IL-2-INDUCIBLE T-CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
1781	1awo		459	508	1.2e-11	-0.29	0.92		ABL TYROSINE KINASE; CHAIN: NULL;	KINASE KINASE, SH3 DOMAIN, TRANSFERASE, PHOSPHOTRANSFERASE, 2 PROTO-ONCOGENE, MULTIPLE DOMAIN, LEUKEMIA
1781	1bhz	A	459	508	1e-11	-0.27	0.84		ABL TYROSINE KINASE; CHAIN: A, C, E, G; PEPTIDE P41; CHAIN: B, D, F, H;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE), SIGNAL TRANSDUCTION, 2 SH3 DOMAIN
1781	1bul	A	459	508	4.5e-12	-0.27	1.00		HEMOTOIETIC CELL KINASE; CHAIN: A, B, C, D, E, F;	TRANSFERASE TYROSINE-PROTEIN KINASE, TRANSFERASE, SIGNAL TRANSDUCTION, 2 SH3
1781	1ddm	A	48	148	0.003	-0.04	0.63		NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	SIGNALING PROTEIN/TRANSFERASE NAK; COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMMETRIC CELL DIVISION
1781	1efh	A	459	507	6e-11	-0.15	1.00		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF	COMPLEX (SH3 DOMAIN)/VIRAL ENHANCER/ SRC-HOMOLGY 3

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
									PROTEIN; CHAIN: B, D;	DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXXP MOTIF
1781	1fyf	A	457	508	1e-11	0.07	1.00		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3B2-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1781	1gbq	A	454	508	1.4e-12	-0.33	0.84		GRB2; CHAIN: A; SOS-1; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN
1781	1gbr	A	446	510	3e-13	-0.35	0.74		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL, 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
1781	1lck	A	456	581	4.8e-19	-0.41	0.01		P56-LCK= TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPPA;	COMPLEX (KINASE/PEPTIDE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1781	1nlo	C	459	507	3e-11	0.18	1.00		ILCK 14 CHAIN: B; ILCK 15 C-SRC; CHAIN: C; NLI (MN7-MN2-MN1-PLP.P); CHAIN: N;	COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)
1781	1pwt		457	508	3e-10	0.21	1.00		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT; SH3 DOMAIN, CYTOSKELETON
1781	1qef	A	456	581	3.2e-18	-0.31	0.15		HAEMATOPHOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1781	1qlw	A	457	508	1.5e-10	0.20	1.00		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON; MEMBRANE, SH3 DOMAIN
1781	1qly	A	455	508	3e-12	-0.05	0.81		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1781	1shf	A	459	508	7.5e-11	-0.64	1.00		PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (B.C.2.7.1.12) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1781	2amb	A	27	153	3e-12	0.25	0.64		NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	CELL CYCLE/GENE REGULATION TRANSDUCTION, COMPLEX, SIGNAL, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETRIC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION
1781	4hck		455	508	7.5e-12	0.46	1.00		HAEMATOPHOETIC CELL	TRANSFERASE HCK; SH3, PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									KINASE; CHAIN: NULL;	TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
1782	1bg1	A	36	198	1.1e-07	0.07	0.04		STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	COMPLEX (TRANSCRIPTION FACTOR/DNA) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION FACTOR/DNA)
1782	1bz4	A	9	126	1.6e-05	0.20	0.04		APOLIPOPROTEIN E; CHAIN: A;	LIPID BINDING PROTEIN APO-E3; LIPID TRANSPORT, LIPID TRANSPORT, HEPARIN-BINDING, PLASMA 2 PROTEIN, HDL, VLDL, REMARK
1782	1cum	A	24	259	3e-13	0.04	-0.06		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2. TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1782	1dn1	B	78	298	7.5e-19	-0.22	0.30		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1782	1ez3	A	118	260	4.5e-07	0.11	0.28		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1782	1ez3	A	138	298	1.5e-08	-0.41	0.00		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1782	1ez3	A	246	394	1e-09	-0.04	0.18		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE



SEQ ID NO:	PDB ID	CHAI ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1782	1fio	A	283	485	7.5e-07	-0.09	0.04		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1782	1fio	A	59	280	1e-11	-0.28	0.03		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1783	1aab		716	763	0.00012	-0.24	0.03		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMGB-BOX DOMAIN A OF RAT HMGI; 1AAB 8 HMGB-BOX 1AAB 20
1783	1dg3	A	2237	2333	4.5e-05	0.02	0.19		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE-BINDING PROTEIN 1; GTP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
1783	1f5n	A	2237	2333	0.00015	0.02	0.04		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GTP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, GMPNP, GPPNP
1783	1fag		69	99	0.003	-0.40	0.03		RAF-1; CHAIN: NULL;	SERINE/THREONINE PROTEIN KINASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, 2 PROTO-ONCOGENE, ZINC, ATP-BINDING, PHORBOL-ESTER BINDING
1783	1hne		716	763	0.0045	-0.29	0.00		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA-BINDING HMGE 3 HMGB-BOX DOMAIN B OF RAT HMGI) (NMR, 1 STRUCTURE) 1HME 4	
1783	1ncf	A	17	141	0.006	0.02	0.12		TUMOR NECROSIS FACTOR RECEPTOR; 1NCF 4 CHAIN: A;	SIGNALING PROTEIN TYPE I RECEPTOR, STNFR1; 1NCF 8

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1783	1ptq		21	50	0.003	0.02	0.23		B; INCF 5	BINDING PROTEIN, CYTOKINE INCF 19
1783	1ltn		21	50	0.00075	-0.09	0.31		PROTEIN KINASE C DELTA TYPE; IPTQ 4	PHOSPHOTRANSFERASE
									PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE
1783	1ltn		69	99	0.006	-0.35	0.41		PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE
1783	2laf	A	716	763	7.5e-05	-0.13	0.31		LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A; DNA (5'-CHAIN: B; DNA (5'-CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1 HMG, TCR-A TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
1784	1ltn		100	137	0.0009	-0.65	0.01		PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE
1785	1alh	A	62	130	3.2e-26	-0.30	0.45		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B; C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1785	1lbo		178	232	3.2e-12	0.07	-0.13		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 111 BB0 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) BB0	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fs Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1785	1bbo		64	113	1.6e-12	-0.88	0.04	4	DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 111 BBBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) BBBO 4	
1785	1mey	C	15	86	1.6e-42	-0.42	0.04		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1785	1mey	C	43	114	4.8e-41	-0.19	0.04		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1785	1mey	G	87	114	3.2e-12	-0.23	0.05		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1785	2adr		62	117	4.8e-18	-0.01	0.90		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION ADR1, ZINC FINGER, NMR
1788	1awc	B	18	157	8e-34	-0.23	0.52		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALP1A; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS.

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1788	1awg	B	3	125	4.8e-29	-0.09	0.29		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION) DNA GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN; ANKYRIN REPEATS, ANKYRIN MOTIF
1788	1bd8		21	160	8e-27	-0.01	0.19		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TRANSCRIPTION 3 FACTOR TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1788	1br7	B	443	560	6.4e-17	0.14	0.04		CYCCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P19INK4A, MTSL; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITOR 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTSL, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1788	1bbx	B	21	160	6.4e-26	-0.17	0.00		CYCCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1788	1bbx	B	50	183	1.3e-23	0.01	0.37		CYCCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1788	1bu9	A	1	130	6.4e-25	-0.12	0.15		CYCCLIN-DEPENDENT KINASE	HORMONE/GROWTH FACTOR P18-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									6 INHIBITOR; CHAIN: A;	INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1788	1d98	A	443	567	1.6e-17	0.14	0.06		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1788	1lhb	A	18	161	1.3e-25	-0.12	0.10		6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1788	1lhb	A	1	129	3.2e-24	0.01	0.37		6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1788	1m70		19	127	1.6e-20	0.14	0.01		MYOTROPIN; CHAIN: NULL	ANK-REPEAT MYOTROPIN, ACETYLATION, NMR, ANK-REPEAT
1791	1b60	A	124	194	1.4e-20	0.17	0.92		UBIQUITIN-LIKE PROTEIN 7, RUB1; CHAIN: A;	SIGNALING PROTEIN RUB1, UBIQUITIN-LIKE PROTEIN, ARABIDOPSIS, SIGNALING PROTEIN
1791	1c3t	A	124	196	1.6e-27	0.02	0.76		1D8 UBIQUITIN; CHAIN: A;	DE NOVO PROTEIN DESIGN, HYDROPHOBIC CORE, PACKING, ROTAMERS, ROC 2, UBIQUITIN, DE NOVO PROTEIN, UBIQUITIN
1791	1n4d	A	124	195	6.4e-20	0.22	0.75		UBIQUITIN-LIKE PROTEIN NEDD8; CHAIN: A, B, C, D;	SIGNALING PROTEIN NEDD8, NEDD8, NEDD8-4, UBIQUITIN-LIKE, PROTEOLYSIS, SIGNALING 2
1791	1lbe	B	124	193	3.2e-27	0.48	0.94		UBIQUITIN TETRAUBIQUITIN 1TBE 3	PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1791	1ubi		124	196	4.8e-29	0.19	0.66		CHROMOSOMAL PROTEIN UBIQUITIN 1UBI 3	
1791	1ud7	A	124	196	3.2e-28	0.39	0.55		UBIQUITIN CORE MUTANT ID7; CHAIN: A;	UBIQUITIN UBIQUITIN, DESIGNED CORE MUTANT
1791	1ueb	A	124	181	6.4e-05	-0.54	0.15		ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;	TRANSCRIPTION TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2 TRANSCRIPTION, TRANSCRIPTIONAL ELONGATION
1792	1bax		1	92	3.2e-36	-0.22	0.64		M-PMV MATRIX PROTEIN; CHAIN: NULL;	MATRIX PROTEIN M-PMV MA
1792	1bax		1	92	3.2e-36			69.49	M-PMV MATRIX PROTEIN; CHAIN: NULL;	MATRIX PROTEIN, CORE PROTEIN, POLYPROTEIN, MYRISTYLATION
1794	1dn1	B	157	227	0.0075	-0.04	0.00		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	MATRIX PROTEIN M-PMV MA
1795	1dn1	B	165	235	0.0075	-0.04	0.00		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	MATRIX PROTEIN, CORE PROTEIN, POLYPROTEIN, MYRISTYLATION
1799	1aj4		225	382	6.4e-36			57.92	TROPONIN C; CHAIN: NULL;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1799	1aj4		241	379	6.4e-36	0.30	0.25		TROPONIN C; CHAIN: NULL;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1799	1ak8		241	309	4.8e-16	0.12	-0.01		CALMODULIN; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PSI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1759	1ap4		241	314	1.4e-12	0.50	-0.01		CARDIAC N-TROPONIN C; CHAIN: NULL;	LOADED, CALCIUM-BINDING PROTEIN
1759	1ani	B	233	391	4.8e-42			69.73	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A; B;	HYDROLASE, CALCIUM-BINDING, IMMUNOSUPPRESSION
1759	1ani	B	240	378	4.8e-42	0.46	0.68		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A; B;	HYDROLASE, CALCIUM-BINDING, IMMUNOSUPPRESSION
1759	1bjf	A	202	345	3.2e-11	-0.02	0.19		NEUROCALCIN DELTA; CHAIN: A; B;	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
1759	1bjf	A	224	385	6.4e-36	0.64	0.83		NEUROCALCIN DELTA; CHAIN: A; B;	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
1759	1bjf	A	224	390	6.4e-36			59.92	NEUROCALCIN DELTA; CHAIN: A; B;	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
1759	1odm	A	241	378	3.2e-42	0.25	0.18		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
1759	1ell		241	378	3.2e-47	0.05	0.21		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)	
1759	1ell		241	380	3.2e-47			59.19	CALCIUM-BINDING PROTEIN	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
			242	309	4.8e-11	0.73	0.13		CALMODULIN (VERTEBRATE); ICLE 3	
1799	1cmf								CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9
1799	1cmf		310	378	1.6e-25	0.43	-0.06		CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9
1799	1dev	A	241	388	3.2e-20	0.01	0.60		APO CIB; CHAIN: A	BLOOD CLOTTING HELICAL, EF-HAND, BLOOD CLOTTING
1799	1ddl	A	183	306	1.4e-12	0.06	0.07		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1799	1ddl	A	241	379	8e-36	0.16	0.69		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1799	1exr	A	241	378	1.3e-44	0.13	0.12		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1799	1771	A	247	309	8e-11	0.40	0.60		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1799	1771	A	316	378	3.2e-24	0.44	0.16		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1799	1i55	A	238	306	9.6e-10	0.25	0.21		TROPONIN C; CHAIN: A;	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCIUM BINDING PROTEIN
1799	1i55	A	313	379	1.3e-19	0.10	0.18		TROPONIN C; CHAIN: A;	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCIUM BINDING PROTEIN
1799	1ipw	A	221	341	3.2e-15	0.18	0.03		CALCIUM-BINDING PROTEIN NCS-1; CHAIN: A;	METAL BINDING PROTEIN YEAST FREQUENTIN EF-HAND, CALCIUM
1799	1jba	A	241	392	1.6e-29	0.46	0.99		GUANYLATE CYCLASE ACTIVATING PROTEIN 2;	LYASE GCAP-2; EF-HAND, CALCIUM-BINDING PROTEIN



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1799	1lef		232	378	3.2e-37	0.10	0.48		CHAIN: A; TROPONIN C; CHAIN: NULL;	GUANYLYL CYCLASE 2 REGULATION CALCIUM-REGULATED MUSCLE CONTRACTION CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1799	1lef		233	379	3.2e-37			63.35	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1799	1ltx		233	378	4.8e-36			61.69	TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND ITNX 14
1799	1ltx		236	378	4.8e-36	-0.22	0.05		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND ITNX 14
1799	1top		227	382	3.2e-38			64.51	CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1799	1top		236	378	3.2e-38	0.02	0.41		CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1799	1lrc	A	242	306	6.4e-11	0.28	-0.05		CALCIUM BINDING PROTEIN CALMODULIN (TR-2-C3) FRAGMENT COMPRISING RESIDUES 78 - 148 (TRC 3 OF THE INTACT MOLECULE) ITRC 4	
1799	1lrc	A	314	378	1.1e-24	0.03	-0.09		CALCIUM BINDING PROTEIN CALMODULIN (TR-2-C3)	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END A.A	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FRAGMENT COMPRISING RESIDUES 78 - 148 ITRC 3 OF THE INTACT MOLECULE) ITRC 4	
1799	1vrk	A	180	309	1.6e-14	-0.21	0.07		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1799	1vrk	A	239	381	3.2e-46			56.76	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1799	1vrk	A	241	378	3.2e-46	0.12	0.33		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1799	1wdc	C	241	382	1.4e-20	0.23	0.04		SCALLOP MYOSIN; CHAIN: A; B, C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1799	3cm		238	306	9.6e-10	0.36	0.13		TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN
1799	3cm		313	379	1.3e-19	0.19	0.12		TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN
1801	1alh	A	120	210	1.6e-12	0.03	0.35		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	138	238	4.8e-19	0.03	0.98		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

SKQ ID NO:	PDB ID	CHAIN	STAR T AA	END AA	PstBlast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1801	1alh	A	214	296	4.5-37			84.50	QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	270	377	1.1-29	0.23	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	270	377	9.6-22	-0.16	0.41		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	298	404	1.6-19	0.22	0.57		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	298	454	3e-19	0.11	0.65		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	353	481	3e-21	0.07	0.78		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	382	481	3.2e-26	0.17	0.15		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	429	509	8e-30	0.45	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	429	510	9e-31	0.54	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1801	1alh	A	457	537	1.1e-30	-0.09	1.00		OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	ZINC FINGER, DNA-BINDING PROTEIN COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	485	565	7.5e-34	0.28	1.00		OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1mey	C	119	210	8e-30	0.10	0.35		OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	157	238	1.4e-37	0.42	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	185	266	3.2e-47	0.55	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	213	294	3.2e-48	0.35	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	241	322	4.8e-49	0.56	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
1801	1mcy	C	241	323	4.8e-49			101.14	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mcy	C	269	377	4.8e-40	-0.06	0.51		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mcy	C	297	453	1.1e-20	0.01	-0.17		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mcy	C	353	481	1.3e-22	0.42	0.70		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mcy	C	357	453	8e-41	0.41	0.24		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mcy	C	381	481	3.2e-45	0.26	0.07		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mcy	C	428	509	1.6e-49	0.51	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1801	1mev	C	456	537	1.6e-49	-0.03	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mev	C	484	565	1.6e-49	0.25	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1u13	A	382	481	6.4e-17	0.23	-0.01		TRANSCRIPTION FACTOR IIIA; CHAIN: A-5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TETRA: 5S GENE; NMR, TETRA, PROTEIN, DNA, TRANSCRIPTION FACTOR; 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1801	1tff6	A	112	247	1.4e-22	0.08	0.22		TETRA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1801	1tff6	A	157	325	3e-61			114.65	TETRA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END A AA	PsiBlast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1801	1t16	A	158	303	9.6-31	0.37	0.99		TH1A; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1801	1t16	A	186	324	1.4-35	0.15	1.00		TH1A; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1801	1t16	A	298	495	1.3-25	0.04	0.24		TH1A; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1801	1t16	A	382	547	1.3-34	-0.15	0.28		TH1A; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1801	1t16	A	429	565	1.6-35	0.23	0.99		TH1A; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1801	1ubd	C	157	266	6e-43	0.25	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT; YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	159	267	7.5e-48			92.90	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	186	294	7.5e-48	0.35	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	217	322	7.5e-51	0.15	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	221	322	1.6e-32	0.17	1.00		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	249	377	3.2e-26	-0.16	0.99		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	305	453	1.6e-24	0.04	-0.02		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	351	509	1.5e-30	0.23	0.64		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	360	481	6.4e-29	0.26	0.36		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
									CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1801	1ubd	C	387	509	3.2e-31	0.07	0.65		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1801	1ubd	C	454	565	4.5e-40	0.30	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1801	1ubd	C	464	565	8e-34	-0.10	0.98		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1801	2drp	A	294	377	3e-18	0.53	0.10		COMPLEX (TRANSCRIPTION) REGULATION(DNA) TRANSCRIPTION INITIATION, ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1801	2gli	A	157	296	1.1e-58			100.38	DNA 2DRP 4 ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	157	296	3e-57	0.25	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	185	322	1.1e-58	0.15	0.90		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	249	404	3.2e-23	0.01	0.81		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	297	511	1.1e-37	0.11	0.49		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	360	508	8e-30	0.15	-0.02		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	424	536	6.4e-32	0.40	0.87		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	428	565	1.5e-48	0.25	0.75		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	436	564	1.6e-33	0.39	0.69		ZINC FINGER PROTEIN GLI1;	COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR ID	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C; D;	PROTEIN(DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1802	1afb	1	89	252	1.5e-21			59.81	MANNULOSE-BINDING PROTEIN-A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB 5	LECTIN CL-OPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22
1802	1b08	A	118	249	3e-31	0.35	0.83		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED-2 COIL, LUNG SURFACTANT, SUGAR BINDING PROTEIN
1802	1b6c		123	253	4.5e-29			74.73	CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
1802	1b6e		126	251	4.5e-29	0.57	0.98		CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
1802	1bj3	A	125	250	8e-25			67.59	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1802	1da8	A	103	249	1.2e-27	0.06	0.18		SURFACTANT PROTEIN A; CHAIN: A;	MEMBRANE PROTEIN SP-A; SP-A-PHOSPHOLIPID MOLECULE COMPLEX
1802	1dv8	A	126	250	1.5e-28	0.47	1.00		ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
1802	1dv8	A	126	252	1.6e-28	0.35	0.48		ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
1802	1e87	A	125	250	1.5e-27	0.79	0.65		EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDUCER MOLECULE (AIM), EA 1, HEMATOPOIETIC CELL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1802	1hnp		98	249	3e-27			63.07	MANNOSE-BINDING PROTEIN; IHUP 4 CHAIN: NULL; IHUP 5	RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE, 2 NKD, KLR
1802	1lxx	A	125	250	1e-24			65.37	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	C-TYPE LECTIN ALPHA-HELICAL COILED-COIL, IHUP 12
1802	1lxx	B	125	252	6e-25			61.47	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING DOMAIN 2 BINDING, C-TYPE CSD MOTIF, LOOP EXCHANGED DIMER
1802	1lit		126	252	3e-25			66.78	LITHOSTATHINE; CHAIN: NULL	COAGULATION FACTOR BINDING DOMAIN 2 BINDING, C-TYPE CSD MOTIF, LOOP EXCHANGED DIMER
1802	1lqdd	A	114	252	3e-28	0.75	0.86		LITHOSTATHINE; CHAIN: A;	PANCREATIC STONE INHIBITOR, LECTIN
1802	1lqdd	A	114	252	3e-28			74.13	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1802	1lqg3	C	123	253	1.5e-30	0.60	0.60		MHC CLASS IIH-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2
										HISTOCOMPATIBILITY, B2M, LY49, LY-49

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1802	1qo3	D	130	253	1.3e-27	0.81	0.43		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YF148, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
1802	1rdl	1	136	251	1.2e-26			61.44	MANNOSE-BINDING PROTEIN-C; 1RDL 6 CHAIN: 1, 2; 1RDL 7	LECTIN SUB-MBP-C; 1RDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1RDL 20
1802	1rtm	1	89	252	4.5e-23			63.45	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) 1RTM 3 1RTM 96	
1802	2a4p	A	123	250	1.3e-29	0.52	0.41		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
1802	2msb	A	136	251	1.3e-25			61.86	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPOLYMER 2MSB 4	
1803	1afb	1	127	291	1.5e-21			60.17	MANNOSE-BINDING PROTEIN-A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB 5	LECTIN CL-OPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22
1803	1b08	A	157	288	3e-31	0.35	0.83		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED-2 COIL, LUNG SURFACTANT, SUGAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verity score	PMF score	SEQFOLD score	Compound	PDB annotation
1803	1b6e		162	292	4.5e-29			75.97	CD94; CHAIN: NULL;	BINDING PROTEIN NK CELL NK CELL RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
1803	1b6e		165	290	4.5e-29	0.57	0.98		CD94; CHAIN: NULL;	NK CELL NK CELL RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
1803	1b6j	A	164	289	1e-24			68.01	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1803	1b6j	A	165	288	1e-24	0.16	0.48		COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1803	1c3a	B	165	290	4.5e-24	0.38	-0.06		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
1803	1du8	A	142	288	1.2e-27	0.06	0.18		SURFACTANT PROTEIN A; CHAIN: A;	MEMBRANE PROTEIN SP-A; SP-A:PHOSPHOLIPID MOLAYLAYER COMPLEX
1803	1dv8	A	165	288	4.8e-25	0.13	0.46		ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
1803	1dv8	A	165	289	1.5e-28	0.47	1.00		ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
1803	1k87	A	164	289	1.5e-27	0.79	0.65		EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDUCER MOLECULE (AIM), EA 1; HEMATOPOIETIC CELL RECEPTOR, LEUCOCYTE, C-TYPE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END A AA	PsI Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1803	1egg	A	165	288	1e-25	0.62	0.95		MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	LECTIN-LIKE 2 NKD, KLR
1803	1hnp		150	288	3e-27			63.43	MANNOSE-BINDING PROTEIN; IHUP 4 CHAIN: NULL; IHUP 5	LECTIN, MANNOSE RECEPTOR C-TYPE LECTIN ALPHA-HELICAL COILED-COIL, IHUP 12
1803	1hnp		164	289	3e-27	0.33	0.40		MANNOSE-BINDING PROTEIN; IHUP 4 CHAIN: NULL; IHUP 5	C-TYPE LECTIN ALPHA-HELICAL COILED-COIL, IHUP 12
1803	1lxx	A	164	289	1e-24			65.74	COAGULATION FACTORS IXA-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IXA-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1803	1lxx	A	165	288	1e-24	0.32	0.48		COAGULATION FACTORS IXA-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IXA-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1803	1lxx	B	164	291	6e-25			61.53	COAGULATION FACTORS IXA-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IXA-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1803	1lxx	B	165	290	6e-25	0.38	0.48		COAGULATION FACTORS IXA-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IXA-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1803	1lit		165	291	3e-25	0.77	0.89		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, LECTIN
1803	1lit		165	291	3e-25			67.30	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, LECTIN
1803	1gdd	A	153	291	3e-28	0.75	0.86		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN



SEQ ID NO:	PDB ID	CHAIN ID	STAR ID	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1803	1qdd	A	153	291	3e-28			73.96	LITHOSTATHINE; CHAIN: A;	PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1803	1qo3	C	162	292	1.5e-30	0.60	0.60		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
1803	1qo3	D	169	292	1.3e-27	0.81	0.43		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
1803	1rdl	I	175	290	1.2e-26			61.70	MANNOSE-BINDING PROTEIN-C; 1RDL 6 CHAIN: 1, 2; 1RDL 7	LECTIN SUB-MBP-C; 1RDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1RDL 20
1803	1rdl	I	176	289	1.2e-26	0.41	0.70		MANNOSE-BINDING PROTEIN-C; 1RDL 6 CHAIN: 1, 2; 1RDL 7	LECTIN SUB-MBP-C; 1RDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1RDL 20
1803	1rtm	I	127	291	4.5e-23			64.49	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) 1RTM	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1803	2afp	A	162	289	1.3e-29	0.52	0.41		3 RTM 96 SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
1803	2msb	A	175	290	1.3e-25			61.86	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPOLYMER 2MSB 4	
1803	2msb	A	176	288	1.3e-25	0.57	0.54		LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPOLYMER 2MSB 4	
1804	1aui	B	1	80	4.8e-24	0.10	0.87		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A; B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1804	1cdm	A	1	81	1.6e-29	-0.07	0.36		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
1804	1cll	1	1	81	8e-36	-0.04	0.49		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1804	1cmf	8		81	8e-32	0.23	0.60		CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; ICMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO T32C-DOMAIN; ICMF 9
1804	1exr	A	1	81	9.6e-34	0.11	0.93		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN; HIGH RESOLUTION, DISORDER

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1804	1l71	A	14	81	8e-30	0.39	0.89		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1804	1lcf		1	81	1.6e-24	0.23	1.00		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1804	1ltp		1	81	1.6e-24	0.25	0.95		CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1804	1lrc	A	12	81	1.4e-30	0.52	0.98		CALCIUM BINDING PROTEIN CALMODULIN / IIR-2-CS FRAGMENT COMPRISING RESIDUES 78-148 ITRC 3 OF THE INTACT MOLECULE ITRC 4	
1804	1vrk	A	1	82	3.2e-35	0.30	0.98		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX (CALCIUM-BINDING PROTEIN/PEPTIDE)
1806	1a9n	A	114	250	8e-24	0.60	1.00		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A; CHAIN: A, C; U2 B; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNNP RIBONUCLEOPROTEIN
1806	1e9n	C	114	250	8e-24	0.58	0.99		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A; CHAIN: A, C; U2 B; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNNP RIBONUCLEOPROTEIN
1806	1d0b	A	44	227	6.4e-34	0.57	0.98		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQOL D score	Coumpound	PDB annotation
1806	1d0b	A	92	235	1.3e-32	0.39	1.00		INTERNALIN B; CHAIN: A;	ADHESION CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1806	1dee	A	132	249	3.2e-25	0.51	0.99		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A <sup>2</sup> RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1806	1dee	A	84	207	3.2e-17	0.45	0.88		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A <sup>2</sup> RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1806	1ds9	A	111	191	3e-14	-0.40	0.78		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2
1806	1ds9	A	125	251	1.6e-28	-0.60	0.46		OUTER ARM DYNEIN; CHAIN: A;	CHLAMYDOMONAS, FLAGELLA CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2
1806	1ds9	A	73	179	3.2e-13	-0.30	0.01		OUTER ARM DYNEIN; CHAIN: A;	CHLAMYDOMONAS, FLAGELLA CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2
1809	1dkg	A	250	398	0.0015	-0.10	0.11		NUCLEOTIDE EXCHANGE FACTOR GRPE; CHAIN: A, B;	COMPLEX (HSP24/HSP70) HSP70, GRPE, MOLECULAR CHAPERONE, NUCLEOTIDE EXCHANGE 2

SEQ ID NO:	PDB ID	CHAIN ID	SYN T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DNAK; CHAIN: D;	FACTOR, COILED-COIL, COMPLEX (HSP24/HSP70)
1809	1dn1	B	143	367	3e-08	0.06	-0.07		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1809	1qua	A	102	374	7.5e-13	-0.12	0.07		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN (TRIPLE-HELIX COILED COIL); CONTRACTILE PROTEIN
1812	1ses	A	439	528	1.6e-05	0.21	0.28		LIGASE(SYNTHETASE) SERYL-TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) ISLES 3 COMPLEXED WITH SERYL-HYDROXAMATE-AMP ISLES 4	
1814	1qhw	A	32	310	4.5e-10			61.74	PURPLE ACID PHOSPHATASE; CHAIN: A;	HYDROLASE TARTRATE-RESISTANT ACID PHOSPHATASE; METAL PHOSPHATASE, HYDROLASE
1814	1qhw	A	39	239	4.5e-10	-0.19	0.34		PURPLE ACID PHOSPHATASE; CHAIN: A;	HYDROLASE TARTRATE-RESISTANT ACID PHOSPHATASE; METAL PHOSPHATASE, HYDROLASE
1814	1ute	A	28	320	0.00014			63.06	II PURPLE ACID PHOSPHATASE; CHAIN: A;	HYDROLASE UTEROFERRIN, TRAP, PAP, TARTRATE RESISTANT ACID PHOSPHATASE, PURPLE ACID PHOSPHATASE, TARTRATE RESISTANT ACID 2 PHOSPHATASE, METALLOENZYME, UTEROFERRIN, HYDROLASE
1814	4kbp	A	10	247	1.5e-12	0.01	0.52		PURPLE ACID PHOSPHATASE; CHAIN: A, B, C, D;	HYDROLASE (PHOSPHORIC MONOESTER) PURPLE ACID PHOSPHATASE, HYDROLASE (PHOSPHORIC MONOESTER)



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										DOSAGE COMPENSATION
1819	1ek1	A	172	305	3.2e-09	-0.00	-0.14		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1819	1ek1	B	39	69	0.006	-0.84	0.05		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1819	1fez	A	38	143	9e-06	0.20	0.64		PHOSPHONACETALDEHYDE HYDROLASE; CHAIN: A, B, C, D;	HYDROLASE HAD-FAMILY ALPHA/BETA CORE DOMAIN, MG(II) BINDING SITE, 5-2 HELIX BUNDLE
1819	1zm		28	316	3e-10	0.12	-0.19		L-2-HALOACID DEHALOGENASE; CHAIN: NULL;	DEHALOGENASE DEHALOGENASE, HYDROLASE
1820	1bc6		137	219	8e-14	0.05	-0.19		7-FE FERREDOXIN; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, IRON-SULFUR
1820	1bc6		176	254	1.1e-10	0.17	-0.17		7-FE FERREDOXIN; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, IRON-SULFUR
1820	1clf		137	199	1.1e-10	0.43	-0.17		FERREDOXIN; 1CLF 5 CHAIN: NULL 1CLF 6	ELECTRON TRANSPORT (IRON-SULFUR PROTEIN)
1820	1dur	A	137	200	1.6e-11	0.53	-0.12		2(4FE-4S) FERREDOXIN; CHAIN: A	ELECTRON TRANSPORT TWO 4FE-4S CLUSTERS
1820	1e08	A	136	519	6.4e-68	0.37	1.00		[FE]-HYDROGENASE (LARGE SUBUNIT); CHAIN: A; [FE]-HYDROGENASE (SMALL SUBUNIT); CHAIN: D; CYTOCHROME C553; CHAIN: E	HYDROGENASE HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX
1820	1e08	A	173	504	3e-92	0.23	1.00		[FE]-HYDROGENASE (LARGE SUBUNIT); CHAIN: A; [FE]-HYDROGENASE (SMALL SUBUNIT); CHAIN: D; CYTOCHROME C553; CHAIN: E	HYDROGENASE HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1820	1fsh	A	1	574	1.4e-85			232.77	PERIPLASMIC HYDROGENASE I; CHAIN: A;	OXIDOREDUCTASE
1820	1fsh	A	69	572	1.4e-85	0.33	1.00		PERIPLASMIC HYDROGENASE I; CHAIN: A;	OXIDOREDUCTASE
1820	1hfe	L	117	524	4.5e-92			223.69	FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L <sub>n</sub> M <sub>i</sub>	OXIDOREDUCTASE
1820	1hfe	L	122	519	3.2e-68	0.40	1.00		FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L <sub>n</sub> M <sub>i</sub>	HYDROGENASE FE-ONLY
1820	1hfe	L	173	504	4.5e-92	0.61	1.00		FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L <sub>n</sub> M <sub>i</sub>	HYDROGENASE, X-RAY
1821	1cum	A	104	344	6e-09	-0.18	0.01		ALPHA SPECTRIN; CHAIN: A, B, C;	CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERIPLASM
1821	1cum	A	51	207	1.5e-07	-0.09	0.36		ALPHA SPECTRIN; CHAIN: A, B, C;	HYDROGENASE FE-ONLY
1821	1quu	A	54	302	9e-12			52.84	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HYDROGENASE, X-RAY
1821	1quu	A	56	340	9e-12	-0.34	0.43		HUMAN SKELETAL MUSCLE	CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERIPLASM



SEQ ID NO;	PDB ID	CHAIN ID	STAR T.AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ALPHA-ACTININ 2; CHAIN: A;	HELIX COILED COIL, CONTRACTILE PROTEIN
1822	1aut	L	29	125	9e-08			51.57	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE; PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1822	1bx7		45	113	6e-11	1.12	-0.15		HIRUSTASIN; CHAIN: NULL;	ANTI-COAGULANT ANTI-COAGULANT, PEPTIDIC INHIBITORS, CONFORMATIONAL 2 FLEXIBILITY, SERINE PROTEASE INHIBITOR
1822	1c2a	A	36	165	1.4e-26	0.53	-0.03		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
1822	1c2a	A	4	126	1.5e-19	0.87	-0.15		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
1822	1dan	L	2	135	7.5e-13	0.56	-0.19		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYL KETONE, (DIFFERENCES) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1822	1du3	A	2	77	7.5e-11	1.08	-0.18		DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, I, K, L;	APOPTOSIS TRAIL, DR5, COMPLEX
1822	1du3	A	31	125	4.5e-12	0.59	-0.12		DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I, TNF-RELATED	APOPTOSIS TRAIL, DR5, COMPLEX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1822	1dx3	A	9	96	6e-12	1.17	-0.15		APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, J, K, L; DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I, TNR-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, J, K, L; THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-Glu-L-Gly-L-ARM; CHAIN: E, F, G, H;	APOPTOSIS TRAIL, DR5, COMPLEX
1822	1dx5	1	47	155	4.5e-11	0.58	-0.14		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-Glu-L-Gly-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1822	1ehd	A	12	111	1.4e-18	0.49	-0.18		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1822	1ehd	A	4	91	7.5e-19	1.11	-0.12		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1822	1ehd	A	52	141	1.4e-18	1.00	0.16		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1822	1els	A	19	121	1.5e-19	0.87	0.17		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1822	1els	A	4	90	1.2e-19	1.02	-0.11		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1822	1els	A	52	141	1.5e-19	1.08	0.10		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1822	1els	A	75	160	7.5e-17	0.24	-0.17		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQOL ID score	Compound	PDB annotation
1822	1en2	A	12	121	3e-18	0.40	-0.13		CHAIN: A; AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUPERANTIGEN SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1822	1en2	A	2	90	6e-16	1.10	-0.18		AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1822	1en2	A	52	141	3e-21	1.04	0.11		AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1822	1en2	A	62	160	6e-18	0.61	-0.14		AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1822	1ext	A	10	177	7.5e-20			62.34	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1822	1ext	A	12	175	7.5e-20	0.78	-0.14		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1822	1ext	A	3	128	6e-13	0.63	-0.14		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1822	1igr	A	4	178	1.5e-28	0.40	-0.19		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR, HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
1822	1k6		47	178	1.2e-19	0.65	-0.15		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1822	1k6		4	155	7.5e-27	1.13	-0.06		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1822	1k6		4	157	7.5e-27			82.39	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1822	1ncf	A	34	171	1.5e-12			50.41	TUMOR NECROSIS FACTOR RECEPTOR, INCF 4 CHAIN: A;	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1822	1ncf	A	35	155	1.5e-12	0.68	-0.14		B <sub>1</sub> INCF 5	BINDING PROTEIN, CYTOKINE INCF 19
1822	1nub	A	12	171	6e-26	0.10	-0.19		TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN; A <sub>1</sub> B <sub>1</sub> INCF 5	SIGNALLING PROTEIN TYPE 1 RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19
1822	1pfx	L	19	179	3e-23	0.14	-0.20		BASEMENT MEMBRANE PROTEIN BM-40; CHAIN; A <sub>1</sub> B <sub>1</sub>	EXTRACELLULAR MODULE OSTEOONECTIN, SPARG, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, GLYCOPROTEIN, ANTI-ADHESIVE PROTEIN, 2 COLLAGEN BINDING, SITE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODRES
1822	1pfx	L	36	178	3e-23	0.44	-0.20	55.26	FACTOR IXA; CHAIN: C, L <sub>1</sub> ; D <sub>1</sub> PHE-PRO-ARG; CHAIN: I <sub>1</sub>	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIAEFG, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1822	1pfx	L	3	123	9e-14	0.44	-0.20		FACTOR IXA; CHAIN: C, L <sub>1</sub> ; D <sub>1</sub> PHE-PRO-ARG; CHAIN: I <sub>1</sub>	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIAEFG, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										INHIBITOR, HEMOPHILIAE/GF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1822	1skz		22	134	1.2e-18	0.63	0.54		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR; 2 SERINE PROTEASE INHIBITOR; THROMBOSIS
1822	1skz		43	147	7.5e-21	0.57	-0.06		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR; 2 SERINE PROTEASE INHIBITOR; THROMBOSIS
1822	1skz		71	176	7.5e-25	0.03	0.11		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR; 2 SERINE PROTEASE INHIBITOR; THROMBOSIS
1822	1skz		71	180	7.5e-25			63.90	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR; 2 SERINE PROTEASE INHIBITOR; THROMBOSIS
1822	1skz		8	117	1.5e-18	0.61	-0.12		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR; 2 SERINE PROTEASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1822	9wga	A	2	158	6e-30			107.39	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	INHIBITOR, THROMBOSIS
1822	9wga	A	2	160	3e-26	0.57	0.03		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1824	1bx7		50	107	4.5e-20	0.23	0.07		HIRUSTASIN; CHAIN: NULL;	ANTI-COAGULANT ANTI-COAGULANT, PEPTIDIC INHIBITORS, CONFORMATIONAL 2 FLEXIBILITY, SERINE PROTEASE INHIBITOR
1824	1du3	A	49	107	3e-08	0.07	-0.12		DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS-INDUCING LIGAND; CHAIN: D, E, F, J, K, L;	APOPTOSIS TRAIL, DR-5, COMPLEX
1824	1mhu		78	108	9e-16	0.40	1.00		METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMRS) 1MHUA 2	
1824	1mhu		78	108	9e-16			65.07	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMRS) 1MHUA 2	
1824	1mrt		78	108	9e-16	0.49	1.00		METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMRS) 1MRTA 2	
1824	1mrt		78	108	9e-16			63.47	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMRS) 1MRTA 2	
1824	1xka	L	54	106	7.5e-06	0.34	0.10		BLOOD COAGULATION FACTOR Xa; CHAIN: L; C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END .AA	Psi Blast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1824	4mt2		48	108	1.3e-14	-0.09	0.15		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	
1824	4mt2		48	108	1.3e-14			127.57	METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	
1825	1a25	A	355	491	4.8e-42	0.47	1.00		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM-1-PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1825	1a25	A	528	646	3.2e-37	0.27	0.90		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM-1-PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1825	1bor		60	109	0.00075	0.33	0.13		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
1825	1byn	A	355	484	3.2e-46	0.68	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1825	1byn	A	510	639	1.4e-27	0.70	0.98		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1825	1cij	A	366	480	1.1e-12	0.17	0.01		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
1825	1cij	A	526	639	1.2e-15	0.37	0.28		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1825	1djk	A	370	467	4.5e-15	0.19	0.62		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	HYDROLASE LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1825	1djk	A	526	620	6e-13	-0.07	0.12		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1825	1djk	B	370	467	4.5e-15	0.16	0.58		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1825	1dqv	A	357	649	3.2e-88	0.47	1.00		SYNAFTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1825	1dqv	A	512	671	4.8e-33	0.24	0.46		SYNAFTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1825	1dgy	A	354	494	1.3e-45	0.33	0.96		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM4+; PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1825	1dgy	A	510	650	6.4e-40	0.38	0.31		PROTEIN KINASE C, ALPHA	TRANSFERASE CALCIUM4+;



SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									TYPE; CHAIN: A;	PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1825	1g25	A	60	109	0.00045	0.10	0.10		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
1825	1hw		373	480	1.5e-16	-0.18	0.41		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1825	1hw		528	631	7.5e-17	0.31	0.23		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1825	1rmd		40	109	0.003	0.21	0.03		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN VDJJ RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(DJ) RECOMBINATION, ANTIBODY; MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1825	1rsy		347	483	4.8e-46			81.61	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN); (CALB) IRSY 3	
1825	1rsy		355	482	4.8e-46	0.81	1.00		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN); (CALB) IRSY 3	
1825	1rsy		510	636	1.6e-27	0.48	0.96		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN); (CALB) IRSY 3	
1825	1vfy	A	60	91	0.00075	0.04	0.16		PHOSPHATIDYLINOSITOL-3-PHOSPHATE BINDING FYVE	TRANSPORT PROTEIN FYVE DOMAIN, ENDOSOME

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A;	MATURATION, INTRACELLULAR TRAFFICKING, 2 TRANSPORT PROTEIN
1825	1zhd	B	10	120	3e-22	0.40	0.69		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RAECDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1825	1zhd	B	8	131	3e-22			71.27	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RAECDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1825	3rpb	A	357	496	3.2e-29	0.62	1.00		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN
1825	3rpb	A	512	649	1.4e-46	0.53	0.58		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN
										ENDOCYTOSIS/EXOCYTOSIS
1828	1cll		29	169	4.8e-53			69.53	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1828	1vtr	A	26	170	1.1e-60			72.01	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX/CALCIUM-BINDING PROTEIN/PEP TIDE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1833	1aut	L	47	145	1.3e-20			58.73	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1833	1aut	L	73	202	1.3e-20	0.14	-0.17		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1833	1dm	L	152	231	6.4e-16	0.10	0.96		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1833	1dan	L	54	193	1.5e-22			60.57	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1833	1dva	L	152	231	6.4e-16	0.26	0.99		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H; L; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C; D; PEPTIDE E-76; CHAIN: X; Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1833	1emm		149	226	1.3e-15			56.72	FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1833	1ext	A	10	173	9e-14			54.06	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
1833	1fak	L	152	231	6.4e-16	0.44	1.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX SERINE PROTEASE/COFACTOR(LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR(LIGAND)), BLOOD CLOTTING
1833	1ldo		43	205	1e-28	0.52	0.43		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1833	1ldo		95	242	1.1e-20	0.12	-0.01		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1833	1ldo		95	247	1e-28			70.82	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1833	1pfx	L	22	146	6e-35			64.61	FACTOR IXA; CHAIN: C, L, D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPLEX, INHIBITOR, HEMOPHILIA/EGF BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
1833	1pfx	L	54	218	6e-35	0.10	-0.12		FACTOR IXA; CHAIN: C, L, D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPLEX,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
										INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1833	1pfx	L	92	226	6e-29	-0.16	0.07		FACTOR IXA; CHAIN: C, L, D, PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1833	1qfk	L	156	226	1.5e-21	0.07	0.62		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1833	1qfk	L	156	231	6.4e-15	0.30	0.98		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1833	1qfk	L	91	195	7.5e-24			55.94	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1833	1qfk	L	92	207	7.5e-24	0.04	0.18		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									(HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	
1833	1tpg		137	226	1e-23	-0.02	0.63		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
1833	1tpg		43	125	1e-23	0.27	0.19		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
1833	1tpg		72	196	3e-21	0.23	0.16		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
1833	1vap	A	34	130	4.5e-18	0.03	-0.12		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2; LIPID DEGRADATION; HYDROLASE
1833	1nka	L	156	226	3e-18	0.18	0.64		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1833	1xka	L	91	208	1.1e-21			59.27	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1833	1xka	L	92	207	1.1e-21	0.32	0.06		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1833	9wga	A	28	207	7.5e-25			78.80	LICITIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1834	1l88	A	4	320	3e-20	0.11	-0.07		RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1834	1l88	B	4	299	7.5e-18	-0.14	0.10		RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1835	1b7f	A	61	144	1.6e-19	-0.03	0.36		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(p*Gp*Up*Up*Gp*Up*Up*Up* Up*Up*Up*Up*U)-CHAIN: P, Q; N-4 CYTOSINE-SPECIFIC METHYLTRANSFERASE PVU II; CHAIN: A;	RNA-BINDING PROTEIN/RNA TSA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX TRANSFERASE TYPE II DNA- (CYTOSINE: N4) METHYLTRANSFERASE, AMINO 2 METHYLATION, SELENOMETHIONINE, MULTI-WELENGTH ANOMALOUS 3 DIFFRACTION
1835	1b00	A	433	480	4.5e-05	-0.57	0.27			
1835	1evj	A	59	150	6.4e-23	-0.34	0.24		POLYDNYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(p*Ap*Ap*Ap*Ap*Ap*Ap* Ap*Ap*Ap*Ap*Ap*Ap*Ap* O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1835	1evj	B	75	237	3.2e-26	0.05	-0.19		POLYDNYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(p*Ap*Ap*Ap*Ap*Ap*Ap* Ap*Ap*Ap*Ap*Ap*Ap*Ap* O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1835	1d2h	A	424	492	1.2e-14	-0.57	0.17		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B, C, D; HU ANTIGEN C; CHAIN: A;	TRANSFERASE METHYLTRANSFERASE
1835	1d9a	A	72	144	3.2e-17	-0.02	0.16			RNA BINDING PROTEIN RNA-BINDING DOMAIN
1835	1dus	A	421	567	9.6e-20	0.37	0.75		M10682; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN METHANOCOCCUS JANNASCHII
1835	1lfe	A	73	139	1.3e-13	0.19	0.62		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP; RBD; RRM; RNA BINDING DOMAIN; NUCLEOLUS
1835	1g6q	I	402	580	3.2e-11	-0.51	0.03		HNRP ARGININE N-METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERASE SAM-BINDING DOMAIN; BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1835	1g6q	I	420	492	1.3e-13	0.20	0.83		HNRP ARGININE N-METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERASE SAM-BINDING DOMAIN; BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1835	1hd1	A	74	144	3.2e-23	0.27	0.06		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D2; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1835	1qtm	A	410	592	6e-21	-0.06	0.58		ERM C METHYLTRANSFERASE; CHAIN: A;	TRANSFERASE RNA METHYLTRANSFERASE ERM C, COFACTOR ANALOGS
1835	1qtm	A	413	524	6.4e-05	-0.12	0.05		ERM C METHYLTRANSFERASE; CHAIN: A;	TRANSFERASE RNA METHYLTRANSFERASE ERM C, COFACTOR ANALOGS
1835	1vid		424	538	1.5e-15	0.23	0.66		CATECHOL O-METHYLTRANSFERASE; CHAIN: NULL;	TRANSFERASE (METHYLTRANSFERASE) COMT; TRANSFERASE METHYLTRANSFERASE, NEUROTANSITTER
1835	1xva	A	426	492	1.5e-10	-0.47	0.05		GLYCINE N-METHYLTRANSFERASE;	METHYLTRANSFERASE GNMT, S-ADENOSYL-L-METHIONINE;



SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi-Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1835	2msx	A	74	144	4.8e-18	-0.04	0.00		CHAIN: A, B; MUSASHI; CHAIN: A;	GLYCINE METHYLTRANSFERASE RNA BINDING PROTEIN RNA-BINDING DOMAIN
1835	2sx1		73	152	8e-18	0.04	0.35		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1835	3sx1	A	61	137	8e-18	0.10	-0.05		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1836	1buo	A	4	85	3.2e-16	0.37	-0.05		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1836	1goi		204	505	1.6e-06	-0.33	0.34		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGOF 3	
1836	1goi		217	450	7.5e-13	-0.42	0.13		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGOF 3	
1836	1goi		246	372	1.5e-15	-0.23	0.07		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGOF 3	
1837	1dm	L	285	370	4.8e-10	-0.00	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									SOLUBLE TISSUE FACTOR; CHAIN: T, I; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1837	1dan	L	361	449	1.1e-12	0.04	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, I; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1837	1dan	L	530	583	3.2e-08	0.21	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, I; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1837	1dva	L	285	370	4.8e-10	0.09	-0.20		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1837	1dva	L	361	449	1.1e-12	0.10	-0.19		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1837	1dva	L	530	583	3.2e-08	0.27	-0.20		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1837	1emn		107	185	1.4e-10	0.19	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1837	1emn		149	227	3.2e-09	0.07	-0.17		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1837	1emn		530	583	4.8e-09	0.03	-0.20		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1837	1f5y	A	102	182	1.6e-11	0.03	-0.20		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING
1837	1f5y	A	143	221	4.8e-09	0.13	-0.20		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING
1837	1fak	L	530	583	3.2e-08	0.22	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H;	BLOOD CLOTTING COMPLEXSERINE PROTEASE(COFACTOR/LQAND), BLOOD COAGULATION, 2 SERINE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, BGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
1837	1pfx	L	328	409	1.1e-12	0.22	-0.13		FACTOR IXA; CHAIN: C, L, D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1837	1pfx	L	361	449	1.6e-11	0.16	-0.19		FACTOR IXA; CHAIN: C, L, D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1837	1qfk	L	152	243	4.8e-10	0.03	-0.15		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRYPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1837	1qfk	L	365	449	6.4e-12	0.02	-0.19		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRYPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1837	1qfk	L	550	583	3.2e-08	0.08	-0.20		COAGULATION FACTOR VIIA	SERINE PROTEASE FVIIA; FVIIA;

SEQ NO:	PDB ID	CIAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									(LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPETIDYL INHIBITOR; CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE
1837	1vmo	A	303	470	3e-15	0.19	-0.19		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN 1 LYMO 3	
1837	1xka	L	530	585	1.6e-08	0.22	-0.20		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2
1837	1xka	L	73	158	4.8e-11	0.04	-0.20		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1837	9wga	A	250	403	9.6e-16	0.21	-0.14		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1837	9wga	A	275	476	4.8e-16	0.01	-0.14		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1838	1a7a	A	163	207	0.0032	-0.09	0.00		S-ADENOSYLHOMOCYSTEINE HYDROLASE; CHAIN: A, B;	HYDROLASE HYDROLASE, NAD BINDING PROTEIN
1838	1ae1	A	173	215	0.00064	0.34	0.21		TROPINONE REDUCTASE4; CHAIN: A, B;	OXIDOREDUCTASE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T/AA	END AA	Fst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1838	1ae1	B	173	215	0.00064	0.44	0.05		TROPINONE REDUCTASE-4; CHAIN: A, B;	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE
1838	1bdb		173	222	4.8e-05	-0.07	0.25		CIS-BIPHENYL-2,3-DIHYDRODIOL-2,3-DEHYDROGENASE; CHAIN: NULL;	OXIDOREDUCTASE NAD-DEPENDENT OXIDOREDUCTASE, SHORT-CHAIN ALCOHOL 2 DEHYDROGENASE, PCB DEGRADATION
1838	1eld	A	173	221	0.00013	0.67	0.89		L-PHENYLALANINE DEHYDROGENASE; CHAIN: A; L-PHENYLALANINE DEHYDROGENASE; CHAIN: B; ALCOHOL DEHYDROGENASE; ICDO 6 CHAIN: A, B; ICDO 7	OXIDOREDUCTASE AMINO ACID DEHYDROGENASE, OXIDATIVE DEAMINATION MECHANISM, 2 OXIDOREDUCTASE
1838	1edo	A	1	367	1.3e-76		56.21		ALCOHOL DEHYDROGENASE; ICDO 6 CHAIN: A, B; ICDO 7	OXIDOREDUCTASE (CH-OH(D)-NAD(+)) OXIDOREDUCTASE ICDO 15
1838	1edo	A	25	366	1.3e-76	0.64	1.00		ALCOHOL DEHYDROGENASE; ICDO 6 CHAIN: A, B; ICDO 7	OXIDOREDUCTASE (CH-OH(D)-NAD(+)) OXIDOREDUCTASE ICDO 15
1838	1eyd	A	173	261	3.2e-05	0.19	0.03		CARBONYL REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE, OXIDOREDUCTASE
1838	1dit	A	1	367	4.8e-75		64.19		ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DINUCLEOTIDE FOLD
1838	1dit	A	26	366	4.8e-75	0.81	1.00		ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DINUCLEOTIDE FOLD
1838	1deh	A	25	366	3.2e-81	0.63	1.00		HUMAN BETA1 ALCOHOL DEHYDROGENASE, 1DEH 7	OXIDOREDUCTASE BETA1 ADH; 1DEH 9 NAD+-DEPENDENT

SEQ ID NO:	PDB ID	CLAI N ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1838	1dth	A	3	367	3.2e-81			74.95	CHAIN: A, B; IDEH 8 HUMAN BETA1 ALCOHOL DEHYDROGENASE; IDEH 7 CHAIN: A, B; IDEH 8	ALCOHOL DEHYDROGENASE IDEH 26 OXIDOREDUCTASE BETA1 ADH; IDEH 9 NAD+ DEPENDENT ALCOHOL DEHYDROGENASE IDEH 26
1838	1e3f	A	26	366	1.6e-69	0.77	1.00		ALCOHOL DEHYDROGENASE, CLASS II; CHAIN: A, B;	ALCOHOL DEHYDROGENASE
1838	1ee2	A	25	366	4.8e-77	0.73	1.00		ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE DEHYDROGENASE, ALCOHOL, NICOTINAMIDE COENZYME, STERIOD 2 BINDING
1838	1hde	A	173	284	9.6e-07	-0.03	0.45		OXIDOREDUCTASE 3-ALPHA, 20-BETA-HYDROXYSTERIOD DEHYDROGENASE (E.C.1.1.1.55) HDG 3 COMPLEXED WITH CARBENOXOLONE HDG 4	
1838	1kev	A	24	369	1.6e-51			53.09	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE OXIDOREDUCTASE, ZINC, NADP
1838	1kev	A	50	367	1.6e-51	0.59	1.00		NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE OXIDOREDUCTASE, ZINC, NADP
1838	1qq8	A	168	207	0.0032	0.28	0.47		FLAVOCYTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A, D;	OXIDOREDUCTASE OXIDOREDUCTASE
1838	1qqr	A	37	370	8e-70			116.09	OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH NADPH 1QQR 3	
1838	1qqr	A	38	367	8e-70	0.75	1.00		OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH NADPH	

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Binst	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1838	1teh	A	1	367	1.6e-86			72.11	100R 3 HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD+ DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE
1838	1teh	A	27	366	1.6e-86	0.60	1.00		HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD+ DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE
1838	1vid		164	268	0.0009	0.51	0.47		CATECHOL O-METHYLTRANSFERASE; CHAIN: NULL;	TRANSFERASE (METHYLTRANSFERASE) COMIT; TRANSFERASE, METHYLTRANSFERASE, NEUROTROPHIC DEGRADATION
1838	1ybv	A	173	280	9.6e-05	-0.20	0.49		TRIHYDROXYNAPHTHALENE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE NAPHTHOL REDUCTASE; OXIDOREDUCTASE
1838	1ykf	A	24	370	4.8e-54			52.30	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE
1838	1ykf	A	52	367	4.8e-54	0.56	1.00		NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE OXIDOREDUCTASE
1839	1ad6		71	349	9.6e-09			52.68	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE;	KINASE KINASE, SIGNAL TRANSDUCTION,



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1839	1b6c	B	50	350	1.1e-15			38.79	CHAIN: NULL; FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	CALCIUM/CALMODULIN COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1839	1b6c	B	70	199	1.5e-13	-0.17	0.06		FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1839	1byg	A	73	337	3.2e-27			62.43	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUFOSPORINE, TRANSFERASE
1839	1byg	A	78	197	1.5e-13	-0.33	0.00		C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUFOSPORINE, TRANSFERASE
1839	1byg	A	87	334	3.2e-27	-0.39	0.01		C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUFOSPORINE, TRANSFERASE
1839	1lgt	A	64	339	1.1e-26			70.22	TGF RECEPTOR I; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1C; FIBROBLAST GROWTH FACTOR RECEPTOR I; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1839	1fgk	B	63	338	3.2e-26			71.37	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1839	1fgk	B	87	335	3.2e-26	0.11	0.41		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1839	1fpu	A	84	332	1.6e-27	-0.20	0.10		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STL-571, ACTIVATION LOOP
1839	1hcl		79	321	1.4e-22	-0.13	0.33		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1839	1lr3	A	63	350	3.2e-26			61.82	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION
										PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1839	1lr3	A	87	332	3.2e-26	0.10	0.16		INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN:	COMPLEX (TRANSFERASE/SUBSTRATE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									B <sub>2</sub>	TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1839	1qdf	A	84	347	1.1e-24	-0.26	0.29		HAEMATOPHOETIC CELL KINASE (HCK); CHAIN: A <sub>2</sub>	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, 2 DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1839	1vr2	A	87	336	1.6e-20	-0.38	0.03		VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A <sub>2</sub>	TRANSFERASE KDR, TYROSINE KINASE
1840	1c1g	A	2	176	8e-09	0.14	-0.20		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1840	1req	A	2	164	1.3e-08	0.19	-0.13		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D; TRANSUDUCIN; CHAIN: B, G; PHOSUDUCIN; CHAIN: P;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE COMPLEX (TRANSDUCER/TRANSDUCTION)
1840	2irc	P	6	112	4.5e-09	0.53	-0.19			GT BETA-GAMMA; MEKA, P33; PHOSUDUCIN, TRANSUDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
1841	1alh	A	117	191	8e-23	-0.46	0.00		QSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1841	1alh	A	166	249	6.4e-30			75.37	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1841	1alh	A	167	247	6.4e-30	-0.18	0.93		QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1841	1alh	A	195	281	3.2e-26	0.06	0.25		QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1841	1alh	A	325	400	6.4e-24	-0.34	0.33		QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1841	1alh	A	348	428	6.4e-30	-0.66	0.87		QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1841	1ard		348	376	1.6e-06	-0.12	0.81		TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADRI (RESIDUES 102 - 130) IARD 3 (AMINO TERMINAL ZINC FINGER DOMAIN) (NMR, 10 STRUCTURES) IARD 4 (ADRI) IARD 5	
1841	1mey	C	109	191	1.6e-38	-0.12	0.22		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION; PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fa Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1841	1mcy	C	138	219	1.6e-47	-0.01	0.98		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mcy	C	166	247	1.6e-48	0.11	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mcy	C	166	248	1.6e-48			83.84	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mcy	C	194	282	8e-45	-0.14	0.22		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mcy	C	324	400	1.1e-41	-0.60	0.22		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mcy	C	347	428	1.6e-45	-0.19	0.82		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mcy	G	220	247	1.1e-12	0.13	0.70		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQVOL D score	Compound	PDB annotation
1841	1mcy	G	345	372	6.4e-13	-0.26	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA) ZINC COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mcy	G	401	428	1.6e-13	0.03	0.48		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1p2		348	376	8e-09	-0.21	0.03		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1841	1d3	A	195	267	1.1e-20	0.03	-0.11		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TTIIA; 5S GENE; NMR, TTIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1841	1d6	A	112	278	3.2e-33			74.20	TTIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1841	1d6	A	139	284	3.2e-33	-0.25	0.49		TTIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1841	1ub6	A	297	437	4.8e-31	-0.30	0.19		TEIIIA; CHAIN: A, D, S; RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1841	1ub6	A	348	488	6.4e-34	-0.37	0.04		TEIIIA; CHAIN: A, D, S; RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1841	1ubd	C	109	219	3.2e-30	-0.16	0.19		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1841	1ubd	C	140	248	3e-32			71.97	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1841	1ubd	C	143	247	3e-32	-0.33	0.78		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fs Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1841	1ubd	C	174	281	3.2e-32	-0.25	0.04		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1841	1ubd	C	332	428	6.4e-30	-0.46	0.40		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1841	2drp	A	323	371	4.8e-06	-0.52	0.01		COMPLEX (TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDES) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1841	2gli	A	138	283	1.6e-32			76.50	ZINC FINGER PROTEIN GLI1; CHAIN: A, DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1841	2gli	A	140	252	6e-29	-0.12	0.62		ZINC FINGER PROTEIN GLI1;	COMPLEX (DNA-BINDING PROTEIN/DNA)



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C; D;	PROTEIN/DNA FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1841	2gli	A	146	283	1.6e-32	0.09	-0.05		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1845	1cun	A	511	648	1.5e-09	1.09	-0.17		ALPHA SPECTRIN; CHAIN: A; B; C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEN 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1845	1cun	A	566	798	7.5e-05	0.39	0.00		ALPHA SPECTRIN; CHAIN: A; B; C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEN 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1845	1dn1	B	437	613	4.5e-10	0.41	-0.20		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1 A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1845	1dn1	B	481	642	1.5e-17	0.57	-0.20		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1 A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1845	1dn1	B	513	769	1.5e-11	0.43	-0.17		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1 A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1845	1ez3	A	447	576	1e-09	0.78	-0.19		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNTAXIN-1A; CHAIN: A, B, C; BUNDLE
1845	1ez3	A	485	601	3e-16	0.83	-0.19		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNTAXIN-1A; CHAIN: A, B, C; BUNDLE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.A.A	END A.A	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1845	1ez3	A	511	650	1.5e-16	1.11	-0.20		SYNTAXIN-1A; CHAIN: A, B, C;	BUNDLE ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1845	1ez3	A	526	658	3e-16	0.98	-0.17		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1845	1ez3	A	739	861	4.5e-05	0.21	0.00		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1845	15n	A	485	626	3e-08	0.74	-0.19		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GTP, GTP HYDROLYSIS, GTP, GMP; INTERFERON INDUCED; DYNAMIN 2 RELATED, LARGE GTPASE FAMILY; GMPNP, GPPNP.
1845	1ifo	A	485	642	9e-13	0.55	-0.20		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1845	1iqu	A	460	656	3e-24	0.70	-0.19		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
1845	1req	A	451	746	4.5e-31	0.48	-0.08		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE; INTRAMOLECULAR TRANSFERASE
1845	1sig		485	643	4.5e-18	0.76	-0.15		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1845	1sig		486	677	6e-17	0.40	-0.20		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1845	2trc	P	488	621	1.5e-17	0.22	-0.20		TRANSDUCIN; CHAIN: B, G;	COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PHOSDUCIN; CHAIN: P;	(TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCIN, 2 REGULATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
1845	2irc	P	513	647	1.5e-20	0.29	-0.19		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	(TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCIN, 2 REGULATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
1845	2irc	P	577	746	1.5e-13	0.23	-0.20		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	(TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCIN, 2 REGULATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
1849	1bor		29	55	1.1e-07	-0.68	0.59		TRANSCRIPTION FACTOR PMI; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	FsI Binst	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1849	1ksr		397	500	4.5e-30			64.85	GELATION FACTOR; CHAIN: NULL;	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120
1849	1ksr		398	498	4.5e-30	0.47	0.99		GELATION FACTOR; CHAIN: NULL;	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120
1849	1ksr		398	499	1.3e-19	0.54	1.00		GELATION FACTOR; CHAIN: NULL;	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120
1849	1qth	A	306	515	6e-36			62.06	GELATION FACTOR; CHAIN: B;	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP-2 120
1849	1qth	A	359	494	1.6e-13	0.11	0.95		GELATION FACTOR; CHAIN: B;	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP-2 120
1849	1qth	A	395	528	1.3e-19	0.52	0.96		GELATION FACTOR; CHAIN: B;	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP-2 120
1849	1qth	A	397	528	6e-36	0.52	0.99		GELATION FACTOR; CHAIN: B;	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP-2 120
1850	1dth	A	175	331	7.5e-06	-0.00	0.21		GLYCINE N-	TRANSFERASE

SEQ ID NO.	PDB ID	CHAIN	STAR T.A.A.	END A.A.	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1850	1lus	A	177	294	6.4e-09	0.24	0.01		METHYLTRANSFERASE; CHAIN: A, B, C, D; M0882; CHAIN: A;	METHYLTRANSFERASE
1850	1g6q	1	148	292	1.3e-14	0.11	0.04		HNRNP ARGININE N-METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANASCHII TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1853	1a5e		538	668	4.5e-32	0.39	0.95		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK, REPEAT
1853	1apm	E	1	349	4.5e-30			99.80	TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMPS-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (SC/APKS) IAPM 3 (CATALYTIC SUBUNIT) ALPHA ISOZYME MUTANT WITH SER 139 IAPM 4 REPLACED BY ALA (SI39AS) COMPLEX WITH THE PEPTIDE IAPM 5 INHIBITOR PK(S-24) AND THE DETERGENT MEGA-8 IAPM 6	
1853	1awc	B	447	604	1.5e-36	0.33	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	1awc	B	486	637	7.5e-43	0.55	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DNA; CHAIN: D, E;	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	1awc	B	551	705	1.2e-45			94.92	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	1awc	B	556	704	6.4e-35	0.72	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	1awc	B	584	737	1.2e-45	0.70	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	1awc	B	617	770	1.5e-44	0.60	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1853	1awc	B	651	802	1.5e-42	0.63	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR, COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	1awc	B	656	802	1.6e-32	0.34	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	1awc	B	687	828	3e-35	0.74	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	1b6c	B	26	276	3e-49	0.37	1.00		PK506-BINDING PROTEIN; CHAIN: A, C, E, G, TOP-B SUPERFAMILY RECEPTOR TYPE 1; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) PKB1/2, SERINE/THREONINE-PROTEIN KINASE RECEPTOR M4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1853	1bd8		445	574	4.8e-10	0.37	0.49		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bd8		458	605	4.5e-35	0.66	1.00		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bd8		486	637	1.4e-40	0.58	1.00		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bd8		518	673	1.5e-44	0.76	1.00		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bd8		585	739	6e-42	0.32	1.00		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bd8		652	805	1.5e-40	0.51	1.00		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bix	B	447	610	1.1e-36	0.21	1.00		CYCCLIN-DEPENDENT KINASE 6; CHAIN: A; P19NK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1853	1bix	B	521	673	3e-43	0.77	1.00		CYCCLIN-DEPENDENT KINASE 6; CHAIN: A; P19NK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1853	1bix	B	587	743	1.5e-41	0.63	1.00		CYCCLIN-DEPENDENT KINASE 6; CHAIN: A; P19NK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,



SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1853	1bix	B	651	808	4.5e-41	0.60	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1853	1bu9	A	444	576	8e-09	0.16	0.87		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1853	1bu9	A	486	612	4.5e-33	0.60	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1853	1byg	A	24	276	1.4e-45	0.81	0.98		C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2
1853	1emk	E	1	349	1.5e-30			96.05	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37); 1CMK 4	STAUFOSPORINE, TRANSFERASE
1853	1eqp	E	1	342	1.5e-30			92.53	TRANSFERASE/PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) 1CTP 3 (E.C.2.7.1.37) 1CTP 4 (E.C.2.7.1.37) 1CTP 4	
1853	1d9e	A	478	610	1e-35	0.73	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1853	1d9e	A	510	637	1.5e-33	0.36	1.00		CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1853	1d9s	A	545	673	7.5e-38	0.65	1.00		4 INHIBITOR B; CHAIN: A; CYCLIN-DEPENDENT KINASE	HELIX, ANKYRIN REPEAT
1853	1d9s	A	608	743	9e-37	0.36	1.00		4 INHIBITOR B; CHAIN: A; CYCLIN-DEPENDENT KINASE	HELIX, ANKYRIN REPEAT
1853	1d9s	A	645	773	1.2e-34	0.43	1.00		4 INHIBITOR B; CHAIN: A; CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1853	1d9s	A	677	807	3e-34	0.54	0.92		4 INHIBITOR B; CHAIN: A; CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1853	1dcq	A	513	694	4.5e-32	0.13	0.51		4 INHIBITOR B; CHAIN: A; PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1853	1fgk	A	18	293	1.5e-45			114.87	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1853	1fgk	A	26	276	1.5e-45	0.46	1.00		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1853	1fgk	B	1	292	7.5e-45			112.87	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1853	1fgk	B	26	276	7.5e-43	0.50	1.00		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1853	1fink		26	276	1.2e-46	0.79	1.00		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1853	1fpu	A	49	276	7.5e-43	0.51	1.00		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1853	1hel		19	326	9e-28			92.94	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2, TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1853	1hhb	A	484	608	3e-34	0.36	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1853	1lkn	D	438	647	4.5e-46	0.41	1.00		NE-KAPPA-B P65 SUBUNIT; CHAIN: A; NE-KAPPA-B P50D SUBUNIT; CHAIN: C; LKAPPA-B ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX
1853	1lkn	D	486	680	6e-53	0.41	1.00		NE-KAPPA-B P65 SUBUNIT; CHAIN: A; NE-KAPPA-B P50D SUBUNIT; CHAIN: C; LKAPPA-B	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1853	1lkn	D	551	749	6e-58	0.21	1.00		B-ALPHA; CHAIN: D; NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1853	1lkn	D	584	775	4.5e-52	0.26	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1853	1lkn	D	617	810	1.3e-54	0.15	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1853	1lr3	A	10	306	1.5e-46			114.32	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1853	1lr3	A	26	276	1.5e-46	0.65	1.00		INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1853	1myo		445	523	8e-13	0.46	0.93		MYOTROPIN; CHAIN: NULL	ANK-REPEAT MYOTROPIN
1853	1myo		458	563	9e-23	0.46	1.00		MYOTROPIN; CHAIN: NULL	ACETYLATION, NMR, ANK-REPEAT ANK-REPEAT MYOTROPIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1853	1myo		461	589	8e-16	-0.06	0.46		MYOTROPHIN; CHAIN: NULL	ACETYLATION, NMR, ANK-REPEAT
1853	1myo		521	635	4.5e-32	0.55	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1myo		554	669	1.5e-36	0.44	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1myo		621	735	1.5e-32	0.34	0.99		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1myo		654	768	3e-13	-0.03	0.57		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1myo		684	800	1.5e-30	0.37	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1inf	E	461	637	6e-43	0.50	1.00		NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1853	1inf	E	484	677	3e-50	0.52	1.00		NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1853	1inf	E	549	749	1.2e-53	0.54	1.00		NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1853	1inf	E	581	778	1.5e-53	0.20	1.00		NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1853	1inf	E	616	815	1.5e-53	0.56	1.00		NE-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									NP-KAPPA-B P56; CHAIN: B, D; LKAPPA-B-ALPHA; CHAIN: E, F;	REG/ANK REPEAT COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1853	1p38		4	359	3e-27			92.67	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN- ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1853	1pme		15	358	6e-29			97.49	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1853	1qcf	A	26	276	1.5e-49	0.66	1.00		HAEMATOPHOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1853	1qpe	A	26	276	7.5e-50	0.71	1.00		LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
1853	1sw6	A	466	592	1.5e-17	-0.40	0.10		REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
1853	1sw6	A	512	759	1.5e-40	-0.17	0.00		REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
1853	1yes	B	452	503	3.2e-12	0.27	0.96		P53; CHAIN: A, 53BP2; CHAIN: B;	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3
1853	1yes	B	458	578	6.4e-12	0.31	1.00		P53; CHAIN: A, 53BP2; CHAIN: B;	POLYMERIZATION, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
										P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1853	1yes	B	488	660	6e-33	0.09	0.99		P53; CHAIN: A, 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1853	1yes	B	554	726	1.4e-38	0.26	0.99		P53; CHAIN: A, 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1853	1yes	B	654	809	7.5e-33	-0.13	0.30		P53; CHAIN: A, 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)

SEQ NO:	PDB ID	CHAI ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1853	3erk		5	356	9e-31			107.86	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, FRK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 FRK2
1854	1ely	A	1	171	9.6e-68			83.26	RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1854	1ely	A	1	173	9.6e-68	0.43	1.00		RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1854	1eqq	A	1	173	1.6e-68	0.55	1.00		TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1854	1eqq	A	1	174	1.6e-68			77.02	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1854	1d5c	A	3	171	6.4e-56	0.48	1.00		RAB6 GTPASE, CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G-PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING
1854	1d56	A	1	176	3.2e-53	0.12	0.59		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWICH, PROTEIN-PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN



SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1854	1ek0	A	1	174	6.4e-55	0.31	1.00		GTP-BINDING PROTEIN YPT31; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2 PROTEIN, ENDOCYTOSIS, HYDROLASE
1854	1kao		1	171	4.8e-64	0.49	1.00		RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1854	1kao		1	174	4.8e-64			95.27	RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1854	1mh1		1	174	1.1e-53			52.65	RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
1854	1mh1		2	176	1.1e-53	0.28	0.94		RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
1854	1plj		1	171	4.8e-52	0.37	1.00		ONCOGENE PROTEIN C-H-RAS P21 PROTEIN MUTANT WITH GLY 12 REPLACED BY PRO IPLJ 3 (G12P) COMPLEXED WITH P3-1(2)-NITROPHENYLETHYL- IPLJ 4 GUANOSINE-5'-(B-G-IMIDO)-TRIPHOSPHATE IPLJ 5	
1854	1rrp	C	2	186	4.8e-36			50.36	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
1854	1zbd	A	1	179	8e-59			60.15	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCD, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1854	1zbd	A	4	176	8e-59	0.43	0.96		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCD, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1854	2ngr	A	1	193	3.2e-50			54.33	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE
1854	3arb	A	2	174	1.1e-59			68.59	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1854	3arb	A	4	174	1.1e-59	0.27	0.99		RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1856	1lfe	I	29	72	3.2e-16	-0.71	0.48		ELASTASE; CHAIN: E; ELAFIN; CHAIN: I;	COMPLEX (SERINE PROTEASE/INHIBITOR) SKIN-DERIVED ANTILEUKOPROTEINASE (SCALP); HYDROLASE, SERINE PROTEASE, 3D-STRUCTURE, ZYMOMEN, PANCREAS, 2 SIGNAL, COMPLEX (SERINE PROTEASE/INHIBITOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1856	1lgr	A	32	80	0.0011	-0.54	0.12		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
1856	2rel		20	72	1.6e-17	-0.02	0.46		R-ELAFIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR, R-SERINE PROTEASE INHIBITOR, R-ELAFIN, ELASTASE INHIBITOR
1857	1ely	A	19	177	9.6e-25			30.43	RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONCOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1857	1esx	A	23	185	1.6e-28	-0.14	0.01		HIS-TAGGED TRANSFORMING PROTEIN RHQ(A(0-181); CHAIN: A; PKC; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTI-PALEOL COILED-COIL
1857	1d5c	A	21	183	3.2e-30	-0.22	0.01		RAB6 GTPASE; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G-PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING
1857	1e0s	A	14	191	4.8e-52	0.11	1.00		ADP-RIBOSYLATION FACTOR 6; CHAIN: A;	G-PROTEIN G PROTEIN, RAS, ARF, ARF6, MEMBRANE TRAFFIC
1857	1ek0	A	22	183	3.2e-28	0.06	-0.13		GTP-BINDING PROTEIN YPT31; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G-PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2
1857	1fzq	A	7	190	1.1e-48	0.50	1.00		ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3; CHAIN: A;	PROTEIN, ENDOCYTOSIS, HYDROLASE
1857	1hur	A	6	182	6.4e-57			83.99	HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	SIGNALING PROTEIN ARF-LIKE PROTEIN 3, ARF3; PROTEIN-GDP COMPLEX WITHOUT MAGNESIUM, ARF FAMILY, RAS 2 SUPERFAMILY, G-DOMAIN
1857	1hur	A	6	192	6.4e-57	0.23	0.92		HUMAN ADP-RIBOSYLATION	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKING, NON-MYRISTOYLATED IHUR 16

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1857	1kno		19	186	1.6e-24				FACTOR 1; 1HUR 5 CHAIN: A; B: 1HUR 7 RAP2A; CHAIN: NULL;	BINDING, MEMBRANE TRAFFICKING, NON-MYRISTOYLATED 1HUR 16 GTP-BINDING PROTEIN, GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1857	1kx4	B	23	185	1.6e-27	0.22	-0.03		P50-RHO GAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHO GAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1857	3nrb	A	22	190	3.2e-33	-0.03	0.30		RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1858	1alh	A	52	132	3.2e-30	-0.07	0.28		QQR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1858	1alh	A	76	162	3.2e-31			58.29	QQR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1858	1alh	A	80	160	3.2e-31	0.40	0.51		QQR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1858	1mey	C	107	188	3.2e-50	-0.22	0.09		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1858	1mey	C	51	132	4.8e-50	-0.18	0.17		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1858	1mey	C	79	160	1.4e-50	0.17	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1858	1mey	C	79	161	1.4e-50			62.32	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1858	1rf3	A	80	160	3.2e-20	0.14	0.24		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TEH1A; 5S GENE; NMR, TEH1A, PROTEIN, DNA, TRANSCRIPTION FACTOR, 3S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1858	1ubd	C	56	160	1.3e-34	-0.08	0.39		YY1; CHAIN: G; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1858	2gli	A	11	162	3.2e-33	-0.10	0.10		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1858	2gli	A	51	188	4.8e-34			58.21	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	BINDING PROTEIN/DNA COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1858	2gli	A	59	188	4.8e-34	-0.37	0.11		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1859	1alh	A	115	198	6.4e-29			60.10	QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	1alh	A	117	197	6.4e-29	-0.04	0.78		QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	1alh	A	145	237	4.8e-27	-0.23	0.35		QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	1alh	A	212	273	6.4e-15	0.07	-0.13		QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	1alh	A	96	169	3.2e-25	-0.26	0.10		QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	1mcy	C	116	197	1.6e-50	-0.03	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1859	1mey	C	116	198	1.6e-50			70.79	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1mey	C	144	237	1.3e-46	-0.02	0.43		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1mey	C	172	265	1.1e-33	-0.35	0.12		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1mey	C	85	141	1.4e-26	-0.22	0.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1mey	C	88	169	1.1e-41	-0.10	0.35		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1mey	G	209	237	1.4e-11	-0.11	0.42		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1paa		212	239	8e-06	-0.29	0.81		TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADRI (RESIDUES 130 -	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									159) IPAA.3 (PAPA - CARBOXY TERMINAL ZINC FINGER DOMAIN) MUTANT WITH IPAA 4 PRO 131 REPLACED BY ALA, PRO 133 REPLACED BY ALA, CYS 140 IPAA 5 REPLACED BY ALA (P131AP133A,C140A) (NMR, 10 STRUCTURES) IPAA 6 SP1F2; CHAIN: NULL;	
1859	1sp2		212	239	3.2e-05	-0.25	0.03			ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1859	1hf3	A	105	169	1.1e-16	-0.52	0.00		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1859	1hf3	A	114	201	1.4e-20			55.20	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1859	1hf3	A	117	198	1.4e-20	-0.08	0.48		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1859	1t66	A	105	239	1.4e-28	-0.24	0.10		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	REGULATION/DNA COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1859	1t66	A	117	275	1.1e-28	-0.01	0.33		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1859	1t66	A	50	237	1.1e-28			66.86	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1859	1t66	A	86	178	3.2e-16	-0.25	0.01		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1859	1t66	C	110	220	3e-22	-0.00	0.45		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1859	1ubd	C	152	265	3.2e-22	-0.06	0.07		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1859	1ubd	C	86	198	3.2e-33			68.47	YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1859	1ubd	C	93	197	3.2e-33	-0.27	0.98		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1859	2adr		117	171	3.2e-16	-0.05	0.37		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1859	2git	A	106	199	6.4e-33	-0.22	0.33		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ NO:	PDB ID	CHAI ID	STAR T AA	END AA	Psi Blast	Verfiy score	PMF score	SEQPOL D score	Compound	PDB annotation
1859	2gli	A	83	218	6.4e-33			68.84	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1859	2gli	A	96	217	1.3e-31	0.04	0.04		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1860	1alh	A	371	452	4.8e-32	0.37	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1860	1alh	A	372	453	4.8e-32			69.01	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1860	1alh	A	399	488	3.2e-28	-0.35	0.41		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1860	1buo	A	4	126	1.3e-37	0.40	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION 1
1860	1buo	A	5	126	1.3e-37			64.40	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1860	1uey	C	336	423	1.6e-47	-0.44	0.09		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1860	1uey	C	370	452	1.3e-50	0.14	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1860	1uey	C	370	452	1.3e-50			67.59	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1860	1uey	C	398	488	3.2e-47	-0.16	0.71		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1860	1uf3	A	399	488	3.2e-19	-0.48	0.23		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA, 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1860	1uf6	A	371	490	1.6e-31	-0.38	0.11		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Binst	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										REGULATION(DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1860	1ubd	C	344	448	1.1e-32	-0.05	0.92		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1860	1ubd	C	375	488	6.4e-34	-0.03	0.89		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1860	1ubd	C	406	493	4.8e-24	-0.08	0.10		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1860	2git	A	224	313	1.6e-09	0.05	-0.20		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GULL ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1860	2git	A	319	452	6.4e-34	0.10	0.07		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1860	2gji	A	344	490	1.6e-34	-0.09	0.11		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1861	1e4o	A	470	630	1.6e-13	0.13	0.18		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPER-TERMOSTABLE PROTEIN
1861	1d2m	A	470	630	1.6e-13	0.05	0.46		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1861	1d2m	A	538	662	1.4e-07	-0.11	0.39		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1861	1d9x	A	457	658	6.4e-17	-0.27	0.24		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1861	1huk	A	508	670	9.6e-39	0.23	0.55		EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	TRANSLATION YEAST INITIATION FACTOR 4A, IF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN
1861	1fuu	A	105	321	4.8e-43	0.09	-0.14		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
1861	1fuu	B	313	670	3.2e-91	0.06	0.43		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
1862	1byu	A	14	211	7.5e-64	0.35	1.00		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1862	1byu	A	15	217	7.5e-64			113.24	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SIQFOL D score	Coumpound	PDB annotation
1862	1byu	B	9	211	1.3e-65	0.44	1.00		GTP-BINDING PROTEIN RAN; CHAIN: A; B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1862	1byu	B	9	215	1.3e-65			109.68	GTP-BINDING PROTEIN RAN; CHAIN: A; B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1862	1c1y	A	16	181	8e-65	0.51	1.00		RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1862	1c1y	A	17	181	8e-65			102.67	RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1862	1c1q	A	17	182	6.4e-64	0.65	1.00		TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1862	1c1q	A	17	182	6.4e-64			98.76	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1862	1c1x	A	19	182	3.2e-58			95.76	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
1862	1d5c	A	18	179	3.2e-62	0.56	1.00		RAB6 GTPASE; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G-PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING
1862	1ak0	A	18	179	9.6e-60	0.68	1.00		GTP-BINDING PROTEIN YPT151; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, YPT151, 2 PROTEIN, ENDOCYTOSIS

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	F <sub>51</sub> Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1862	1hr	A	17	187	3e-60			113.50	RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	HYDROLASE SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1862	1hr	A	18	186	3e-60	0.80	1.00		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1862	1kao		17	182	9.6e-59			98.96	RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1862	1rtp	C	15	198	1.4e-60			114.45	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP558; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
1862	1rtp	C	16	193	1.4e-60	0.45	1.00		RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP558; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
1862	1tx4	B	19	180	4.8e-55			87.88	P50-RHO GAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX (GTPASE ACTIVATING PROTEIN) GTPASE-ACTIVATING PROTEIN RHO GAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), COMPLEX (GTPASE, 2 TRANSITION STATE, GAP
1862	1zbd	A	12	187	4.8e-69			130.15	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN,







SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Binst	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										SPlicing INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1365	1ses	A	439	542	3.2e-05	-0.21	0.01		LIGASE(SYNTHETASE) SERYL-TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXYAMATE-AMP 1SES 4	
1367	1xbr	A	1	94	1.6e-21	-0.88	0.60		T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA-BINDING PROTEIN
1367	1xbr	A	1	96	1.2e-37	-0.90	0.47		T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA-BINDING PROTEIN
1370	1a4y	A	183	350	8e-08	0.30	0.43		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1370	1a4y	A	209	338	1.4e-08	0.15	0.60		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1870	1a4y	A	209	373	3e-06	0.14	0.25		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	3 REPEATS COMPLEX (INHIBITOR/NUCLEIC ACID) COMPLEX (INHIBITOR/NUCLEIC ACID) COMPLEX (R-ANG), HYDROLASE 2 MOLECULAR RECOGNITION; EPTOTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1870	1d0b	A	196	333	8e-07	0.40	0.12		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT; CALCIUM BINDING, CELL ADHESION
1870	1d0b	A	222	354	0.00096	-0.10	0.25		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT; CALCIUM BINDING, CELL ADHESION
1870	1f0l	A	193	306	1.1e-06	0.03	0.03		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)
1870	1f0l	B	193	306	1.1e-06	-0.01	0.00		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)
1870	1f0v	A	128	349	1.1e-46	0.45	0.51		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1870	1f62	A	128	349	4.8e-36	0.22	0.72		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1870	1y7g	A	248	347	0.00064	0.09	0.27		GTPASE-ACTIVATING	TRANSCRIPTION RNA IF; RANGAP;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PROTEIN RNAI_SCHPO; CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT, PROTEIN, TWINNING, HEMIFEDRAL TWINNING, 3 MEROFEDRAL TWINNING, MEROFEDRY
1870	2bnh		209	338	3.2e-09	-0.03	0.71		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1871	1bak		168	291	4.8e-10	0.08	-0.03		G-PROTEIN COUPLED RECEPTOR KINASE 2; CHAIN: NULL;	TRANSFERASE GRK-2, BETA-ADRENERGIC RECEPTOR KINASE 1, BETA-ARK PLECKSTRIN HOMOLOG DOMAIN, PH DOMAIN, SIGNAL TRANSDUCTION, 2 G, BETA-GAMMA BINDING DOMAIN, BETA-ADRENERGIC RECEPTOR 3 KINASE, BETA-ARK, G-PROTEIN COUPLED RECEPTOR KINASE (GRK-2)
1871	1bm		172	271	8e-12	0.19	0.96		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
1871	1dre		182	264	1.5e-05	0.22	0.21		BETA-SPECTRIN; IDRO 6 CHAIN: NULL; 1DRO 7	CYTOSKELETON
1871	1dyn	A	186	271	4.8e-10	0.13	0.11		SIGNAL TRANSDUCTION PROTEIN DYNAMIN (PLECKSTRIN HOMOLOG DOMAIN) (IDYNPH) IDYN 3	
1871	1eff	A	149	464	1.6e-58	0.05	0.53		MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL DOMAIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1871	1fao	A	170	269	3.2e-17	0.31	0.80		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAME2, PLECKSTRIN, 3- PHOSPHORINOSITIDES, INOSITOL, TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1871	1f08	A	170	269	3.2e-17	0.14	0.69		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAME2, PLECKSTRIN, 3- PHOSPHORINOSITIDES, INOSITOL, TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1871	1fgv	A	172	272	4.8e-18	0.49	0.65		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
1871	1gc7	A	134	464	3.2e-58	-0.01	0.01		RADIXIN; CHAIN: A;	CELL ADHESION 3 SUBDOMAINS CYTOSKELETON, CELL ADHESION
1871	1pls		169	285	1.4e-14	0.14	0.09		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOG) DOMAIN) MUTANT IPLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105-LEHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	
1872	1a05	A	5	390	0			66.11	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A; B;	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DECARBOXYLATING DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS
1872	1a05	A	8	387	0	0.03	0.54		3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A;	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE,

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									B <sub>1</sub>	DECARBOXYLATING DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS
1872	1ai2		5	387	0	0.01	0.60		ISOCITRATE DEHYDROGENASE, CHAIN: NULL;	OXIDOREDUCTASE OXALOSUCCINATE DECARBOXYLASE, IDH; OXIDOREDUCTASE (NAD(+)-CHOH(D)), NADP, PHOSPHORYLATION, 2 GLYOXYLATE BYPASS
1872	1ai2		7	387	0			62.58	ISOCITRATE DEHYDROGENASE, CHAIN: NULL;	OXIDOREDUCTASE OXALOSUCCINATE DECARBOXYLASE, IDH; OXIDOREDUCTASE (NAD(+)-CHOH(D)), NADP, PHOSPHORYLATION, 2 GLYOXYLATE BYPASS
1872	1cm7	A	1	382	0			63.70	3-ISOPROPYLMALATE DEHYDROGENASE, CHAIN: B <sub>1</sub>	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DEHYDROGENASE, NAD- DEPENDANT ENZYME, 2 LEUCINE BIOSYNTHETIC PATHWAY
1872	1cm7	A	1	389	0	0.04	0.41		3-ISOPROPYLMALATE DEHYDROGENASE, CHAIN: B <sub>1</sub>	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DEHYDROGENASE, NAD- DEPENDANT ENZYME, 2 LEUCINE BIOSYNTHETIC PATHWAY
1872	1enz	A	1	382	0			60.42	3-ISOPROPYLMALATE DEHYDROGENASE, CHAIN: B <sub>1</sub>	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DEHYDROGENASE, LEUCINE BIOSYNTHETIC PATHWAY, 2 NAD- DEPENDANT ENZYME
1872	1enz	A	1	389	0	-0.04	0.65		3-ISOPROPYLMALATE DEHYDROGENASE, CHAIN: A <sub>1</sub>	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									B <sub>2</sub>	DEHYDROGENASE, LEUCINE BIOSYNTHETIC PATHWAY, 2 NAD-DEPENDANT ENZYME
1872	1ldm		42	366	4.8e-95			54.18	3-ISOPROPYLMALATE DEHYDROGENASE; IIDM 5 CHAIN: NULL; IIDM 6	OXIDOREDUCTASE IPMDH; IIDM 7 CHIMERA IIDM 20
1872	1ldm		9	387	4.8e-95	0.06	0.42		3-ISOPROPYLMALATE DEHYDROGENASE; IIDM 5 CHAIN: NULL; IIDM 6	OXIDOREDUCTASE IPMDH; IIDM 7 CHIMERA IIDM 20
1872	1xac		42	366	1.6e-96			50.68	3-ISOPROPYLMALATE DEHYDROGENASE 2T2M6T S82R; 1XAC 8 CHAIN: NULL; 1XAC 9	OXIDOREDUCTASE IPMDH; IMDH; 1XAC 10 OXIDOREDUCTASE, CHIMERA 1XAC 21
1872	1xac		9	387	1.6e-96	0.04	0.46		3-ISOPROPYLMALATE DEHYDROGENASE 2T2M6T S82R; 1XAC 8 CHAIN: NULL; 1XAC 9	OXIDOREDUCTASE IPMDH; IMDH; 1XAC 10 OXIDOREDUCTASE, CHIMERA 1XAC 21
1872	2ayq	A	6	387	0	-0.03	0.57		3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A <sub>2</sub> B <sub>2</sub>	OXIDOREDUCTASE 3-ISOPROPYLMALATE DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS, MODERATE THERMOPHILE
1872	2ayq	A	6	388	0			68.62	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A <sub>2</sub> B <sub>2</sub>	OXIDOREDUCTASE 3-ISOPROPYLMALATE DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS, MODERATE THERMOPHILE
1873	1a5e		10	125	1.6e-23	0.44	0.51		TUMOR SUPPRESSOR P16INKA; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1873	1awe	B	10	156	4.8e-36	0.11	0.22		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Binst	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	REGULATION/DNA) GABP ALPHA; GABP BETA; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1873	1awc	B	2	125	6.4e-33	0.43	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1873	1bd8		13	157	3.2e-32	0.05	0.11		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1873	1bd8		3	128	1.1e-23	0.22	0.96		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1873	1b17	B	10	125	8e-24	0.52	0.62		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16NK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1873	1b1k	B	13	157	8e-33	0.18	0.15		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19NK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1873	1btk	B	3	128	1.6e-22	0.42	0.96		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P18INK4D; CHAIN: B;	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE) COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1873	1bu9	A	10	153	6.4e-34	0.16	0.71		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1873	1bu9	A	2	130	4.8e-27	0.15	0.55		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1873	1bu9	A	10	131	3.2e-24	0.05	0.49		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1873	1lhb	A	10	153	6.4e-34	0.23	0.60		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1873	1lhb	A	2	129	1.6e-26	0.14	0.74		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1873	1myo		11	127	1.3e-24	0.21	0.64		MYOTROPIN; CHAIN: NULL	ANK-REPEAT MYOTROPIN, ACETYLATION, NMS, ANK-REPEAT
1873	1nff	E	4	212	3.2e-40	0.02	0.45		NE-KAPPA-A-B P65; CHAIN: A, C; NE-KAPPA-A-B P50; CHAIN: B, D;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									LKAPPA-B-ALPHA; CHAIN: E; F;	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1874	1a5e		10	120	3.2e-16	0.03	0.81		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1874	1bd8		13	153	3.2e-27	0.03	0.31		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1874	1bd8		2	120	1.4e-15	-0.04	0.01		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1874	1bi7	B	10	120	3.2e-17	0.18	0.68		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1874	1bi7	B	52	153	1.4e-17	0.15	0.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1874	1bx	B	13	153	3.2e-25	0.09	0.31		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blst	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1874	1bkx	B	2	120	1.6e-14	0.08	-0.09		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1874	1bu9	A	13	158	1.3e-29	-0.15	0.23		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1874	1bu9	A	2	125	1.3e-18	0.04	0.11		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1874	1bu9	A	54	212	6.4e-28	0.01	0.05		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1874	1d9s	A	10	120	1.6e-17	0.28	0.33		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1874	1dcq	A	13	122	1.5e-12	0.08	0.69		PKC2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1874	1lhb	A	2	124	4.8e-18	0.40	0.71		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1874	1lib	A	54	211	3.2e-27	-0.09	0.27		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	INHIBITOR CELL CYCLE INHIBITOR P18-INK4CINK9; CELL CYCLE INHIBITOR, P18-INK4CINK6; ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1874	1myo		11	138	1.1e-21	-0.17	0.24		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1874	1myo		73	159	1.1e-21	0.30	0.23		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1874	1yes	B	60	193	4.8e-20	-0.03	0.01		P53; CHAIN: A; 53RP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM; COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1877	1alh	A	239	335	9.6e-26	0.12	0.66		QSKR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1877	1alh	A	243	336	7.5e-29	0.04	0.00		QSKR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1877	1alh	A	283	365	7.5e-29			72.03	QSKR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1877	1alh	A	395	502	1.5e-39	-0.14	0.09		QSKR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
									OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1877	1mev	C	161	263	4.8e-42	-0.16	0.06		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	166	307	1e-11	-0.57	0.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	190	335	3e-26	-0.46	0.37		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	217	307	8e-40	-0.24	0.07		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	266	335	1.3e-39	0.02	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	282	363	6.4e-50	0.29	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	282	364	8e-51			98.03	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	310	391	8e-51	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	338	419	3.2e-51	0.43	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	366	447	1.3e-50	0.28	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	394	473	4.8e-47	0.20	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	422	529	3e-40	-0.02	0.82		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	450	529	3.2e-48	0.39	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mev	C	476	553	8e-34	0.46	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Ψi Blast	Verfiy score	PMF score	SEQFOL D score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mcy	G	187	214	1.6e-11	-0.12	0.48		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mcy	G	236	263	6.4e-12	-0.05	0.52		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1sp2		190	218	9.6e-07	0.02	0.09		SPIF2; CHAIN: NULL;	ZINC FINGER, TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI
1877	1u3	A	239	335	4.8e-17	0.27	0.07		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1877	1u6	A	162	316	8e-31	-0.24	0.11		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2
1877	1u6	A	239	400	9.6e-36	-0.06	0.75		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1877	1t66	A	310	471	7.5e-68			107.85	TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1877	1t66	A	311	454	8e-38	-0.02	0.99		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1877	1t66	A	367	511	4.8e-38	0.12	1.00		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1877	1t66	A	395	531	8e-34	0.17	0.95		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1877	1ubd	C	165	335	1.4e-26	-0.39	0.37		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	C	243	363	7.5e-40	-0.00	0.98		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	C	246	363	6.4e-33	-0.09	0.86		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	C	287	391	3e-50	0.00	1.00		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	C	318	419	3.2e-35	-0.13	0.95		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, B;	INITIATOR ELEMENT <sup>+</sup> , YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	C	340	448	3e-48			86.32	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	C	364	474	1.1e-47	0.26	0.99		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	C	374	473	4.8e-32	0.03	0.95		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	C	392	501	3e-48	0.10	0.99		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1877	1ubd	C	420	530	1.5e-48	0.12	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	C	430	529	8e-34	-0.08	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	2adr		162	216	1.3e-14	-0.48	0.41		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1877	2adr		239	309	1.6e-12	-0.23	0.63		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1877	2gil	A	190	365	1.5e-46	0.15	0.80		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1877	2gil	A	246	390	3.2e-33	0.19	0.41		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1877	2gil	A	282	421	1.5e-66			93.76	ZINC FINGER PROTEIN GLI1;	COMPLEX (DNA-BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1877	2gli	A	310	303	1.5e-66	-0.16	0.27		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1877	2gli	A	395	533	6e-53	-0.16	0.93		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1878	1d2n	A	169	424	3.2e-15			65.03	N-ETHYLMALIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1878	1d2n	A	196	349	3.2e-15	0.35	0.64		N-ETHYLMALIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1878	1e94	E	169	270	3.2e-13	-0.74	0.10		HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLV; CHAIN: E, F;	CHAPERONE HSLV; HSLV CHAPERONE, HSLV, CLPQY, AAA-ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
1878	1fnn	A	184	405	1.5e-15	0.22	0.28		CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	CELL CYCLE CDC6P, CDC6, CDC18, ORC1, AAA PROTEIN, DNA REPLICATION INITIATION 2 FACTOR, CELL CYCLE CONTROL FACTOR
1878	1g41	A	169	360	1.6e-16	0.00	0.57		HEAT SHOCK PROTEIN HSLV; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPQY, ATP-DEPENDENT PROTEOLYSIS
1878	1g41	A	183	442	4.5e-34	0.16	0.23		HEAT SHOCK PROTEIN HSLV; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPQY, ATP-DEPENDENT PROTEOLYSIS
1878	2cmk	A	218	245	0.0045	-0.51	0.15		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1882	1ajs	A	54	499	1.6e-58			77.13	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE CYTOSOLIC ASPARTATE AMINOTRANSFERASE, PIG, IN THE 2 PRESENCE OF LIGAND 2-METHYLASPARTATE, AMINOTRANSFERASE
1882	1ajs	A	89	517	1.6e-58	0.08	0.88		ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE CYTOSOLIC ASPARTATE AMINOTRANSFERASE, PIG, IN THE 2 PRESENCE OF LIGAND 2-METHYLASPARTATE, AMINOTRANSFERASE
1882	1ars		85	457	1.6e-64	-0.19	0.51		TRANSFERASE (AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEXED WITH IARS 3 PYRIDOXAL-5'-PHOSPHATE IARS 4	
1882	1ars		95	508	1.6e-64			76.94	TRANSFERASE (AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEXED WITH IARS 3 PYRIDOXAL-5'-PHOSPHATE IARS 4	
1882	1ax4	A	68	523	4.8e-13			71.45	TRYPTOPHANASE; CHAIN: A, B, C, D;	TRYPTOPHAN BIOSYNTHESIS TRYPTOPHAN INDOLE-LYASE; TRYPTOPHAN BIOSYNTHESIS TRYPTOPHAN INDOLE-LYASE, PYRIDOXAL 2,5-PHOSPHATE, MONOVALENT CATION BINDING SITE
1882	1b8g	A	80	515	0	0.44	1.00		1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE; CHAIN: A, B;	LYASE ACC SYNTHASE, S-ADENOSYL-L-METHIONINE ETHYLENE BIOSYNTHESIS
1882	1b9h	A	181	304	1.6e-10	0.08	0.33		3-AMINO-5-	RIFAMYCIN BIOSYNTHESIS (RIFD)

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HYDROXYBENZOIC ACID SYNTHASE; CHAIN: A;	GENE) AHBA SYNTHASE; RIFAMYCIN BIOSYNTHESIS (RIFD GENE)
1882	1bjw	A	102	515	9.6e-84	0.52	1.00		ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE
1882	1bjw	A	83	514	9.6e-84			134.98	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE, PYRIDOXAL ENZYME
1882	1bw0	A	66	520	1.6e-67	0.24	1.00		TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE, PYRIDOXAL ENZYME
1882	1bw0	A	92	520	1.6e-67			158.29	TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, 2 AMINOTRANSFERASE, 2 PYRIDOXAL-5-PHOSPHATE, PLP
1882	1c7n	A	125	514	6e-52	0.34	1.00		CYSTALYSIN; CHAIN: A, B, C, D, E, F, G, H;	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, 2 AMINOTRANSFERASE, 2 PYRIDOXAL-5-PHOSPHATE, PLP
1882	1cs1	A	144	302	1.6e-08	-0.10	0.13		CYSTATHIONINE GAMMA-SYNTHASE; CHAIN: A, B, C, D;	TRANSFERASE TRANSFERASE, PHOSPHATE
1882	1d2f	A	128	514	4.5e-53	0.35	1.00		MALY PROTEIN; CHAIN: A, B;	LYASE CGS; LYASE, LLP-DEPENDENT ENZYMES, METHIONINE BIOSYNTHESIS
1882	1dfo	A	182	415	4.8e-07	0.42	1.00		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE
1882	1etu	A	123	514	9.6e-13	0.17	0.87		L-CYSTEINE/L-CYSTEINE C-S LYASE; CHAIN: A, B;	AMINOTRANSFERASE FOLD, LARGE PLP-BINDING DOMAIN, SMALL C-2 TERMINAL DOMAIN, OPEN ALPHA-BETA STRUCTURE. TRANSFERASE SHMT; SERINE METHYLASE; ALPHA PLP ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD
										BIOSYNTHESIS, PYRIDOXAL 5'-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										PHOSPHATE, 2 THIOCYSTEINE, AMINOACRYLATE, ENZYME-PRODUCT COMPLEX
1882	1yaa	A	76	516	4.8e-52			79.51	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	AMINOTRANSFERASE
1882	1yaa	A	89	452	4.8e-52	0.06	1.00		ASPARTATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	AMINOTRANSFERASE
1882	2ayl	A	79	488	8e-53			74.67	AROMATIC AMINO ACID AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE AROAT;
1882	2ayl	A	85	457	8e-53	-0.16	0.88		AROMATIC AMINO ACID AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE
1882	2ast	A	81	517	1.6e-58	-0.13	0.95		TRANSFERASE (AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (CASPAT) (E.C.2.6.1.1) 2CST 3 COMPLEXED WITH PYRIDOXAL-5-PHOSPHATE AND MALEATE 2CST 4	AMINOTRANSFERASE
1882	2cst	A	88	499	1.6e-58			75.00	TRANSFERASE (AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (CASPAT) (E.C.2.6.1.1) 2CST 3 COMPLEXED WITH PYRIDOXAL-5-PHOSPHATE AND MALEATE 2CST 4	
1882	2ppl	A	110	508	1.1e-48	0.01	0.34		TYROSINE PHENOL-LYASE; CHAIN: A, B;	LYASE LYASE, PLD-DEPENDENT ENZYME, PYRIDOXAL PHOSPHATE
1882	3tat	A	80	457	9.6e-58	-0.17	0.95		TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F;	AMINOTRANSFERASE PHEAT, TYRAT, AROAT; AMINOTRANSFERASE, AROMATIC



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1882	3tat	A	95	497	9.6e-58			91.42	TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F;	SUBSTRATES, PLP ENZYME AMINOTRANSFERASE PHEAT, TYRAT, AROAT AMINOTRANSFERASE, AROMATIC SUBSTRATES, PLP ENZYME
1882	7aat	A	73	457	6.4e-65	-0.10	0.43		TRANSFERASE (AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEX WITH 7AAT 3 PYRIDOXAL-5'-PHOSPHATE AT PH 7.5 7AAT 4	
1882	7aat	A	88	492	6.4e-65			78.03	TRANSFERASE (AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEX WITH 7AAT 3 PYRIDOXAL-5'-PHOSPHATE AT PH 7.5 7AAT 4	
1883	1lar	B	3	220	1.1e-58	-0.13	0.18		LAR; CHAIN: A, B;	HYDROLASE TYROSINE PHOSPHATASE, LAR PROTEIN
1883	1mkp		52	200	6.4e-24			68.80	PYST1; CHAIN: NULL;	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE
1883	1mkp		55	200	6.4e-24	0.57	1.00		PYST1; CHAIN: NULL;	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE
1883	1vhr	A	37	208	7.5e-31			139.04	HUMAN VHR-RELATED DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B;	HYDROLASE VHR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE
1883	1vhr	A	50	200	7.5e-31	0.74	1.00		HUMAN VHR-RELATED DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B;	HYDROLASE VHR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE
1884	1ae6	H	20	242	9.6e-82	0.30	1.00		ANTIBODY CTM01; CHAIN: L;	IMMUNOGLOBULIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsl Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
	1aiv	H	20	244	8e-84	0.43	1.00		H <sub>2</sub> HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB253 FRAGMENT; CHAIN: H, K, L, M;	IMMUNOGLOBULIN FAB FRAGMENT, HUMANISATION COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
1884	1bd2	E	21	261	1.2e-81			301.81	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1884	1bd2	E	22	261	1.2e-81	0.66	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1884	1bec		21	261	1.5e-76			273.44	14.3.D T CELL ANTIGEN RECEPTOR; IBBC 5 CHAIN: NULL; IBBC 6	RECEPTOR T CELL; RECEPTOR IBEC 14
1884	1d5i	H	20	244	1.3e-81	0.23	0.99		CHIMERIC GERM LINE PRECURSOR OF OXY-COPE CHAIN: L; CHIMERIC GERM LINE PRECURSOR OF OXY-COPE CHAIN: H;	IMMUNE SYSTEM IMMUNE SYSTEM
1884	1e60	H	20	244	4.8e-81	0.40	1.00		IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L; IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H;	IMMUNOGLOBULIN FAB ANTIBODY, ANTIGEN, HIV-1, P24, CA
1884	1fvd	B	20	247	1.1e-84	0.18	1.00		IMMUNOGLOBULIN FAB	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
1384	Igc	H	20	247	1.6e-83	0.22	1.00		COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 F4B FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IGC 5 PROTEIN G, STREPTOCOCCUS IGC 15	
1384	Igt	B	20	282	3.2e-90	-0.00	0.98		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1384	Igy	B	21	282	3.2e-82	0.07	0.82		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1384	Iggp	H	20	244	1.6e-83	0.21	1.00		NI G9 (IGG1-LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN
1384	Iqub	A	12	130	9e-07	0.22	1.00		SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C;	IMMUNOGLOBULIN VARIABLE HEAVY (VH) DOMAIN, VARIABLE LIGHT (VL) ANTIBODY FRAGMENT, MULTIVALENT ANTIBODY, DIABODY, DOMAIN 2 SWAPPING, IMMUNOGLOBULIN
1384	Itr	B	19	262	8e-71		277.99		ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR, T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
1385	Igt1	A	314	369	0.0094	-0.34	0.04		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
1386	Ibuo	A	10	129	4.8e-24	0.34	1.00		PROMYEOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1887	1d8z	A	1342	1410	4.5e-05	0.45	1.00		AP*AP*AP* (A-3); CHAIN: M, N, O, P, Q, R, S, T; HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1887	1l0c	A	1331	1417	3e-05	0.42	0.65		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; KNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1887	1oam	A	14	207	4.5e-09	0.70	-0.20		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
1887	1pho		11	218	7.5e-10	0.77	-0.19		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) (PHO 3	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1887	1qo4	A	37	204	4.5e-08	0.89	-0.19		CHAIN: A;	
1887	1sxl		1325	1396	0.00015	0.07	0.54		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	
1887	2axl		1339	1410	0.00015	0.47	1.00		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1887	2u2f	A	1342	1410	1.3e-05	0.44	0.99		SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN
1887	3sxl	A	1339	1432	6e-05	0.01	0.55		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2





SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Coumpound	PDB annotation
1889	1evj	B	1243	1313	3<-05	0.41	0.89		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-RC <sup>+</sup> AP <sup>+</sup> AP <sup>+</sup> AP <sup>+</sup> AP <sup>+</sup> AP <sup>+</sup> AP <sup>+</sup> AP <sup>+</sup> AP <sup>+</sup> AP <sup>+</sup> A) <sup>3</sup> ; CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PAPB 1; REM, REGULATION-RNA COMPLEX, GENE REGULATION/RNA
1889	1d8z	A	1245	1313	4.5e-05	0.45	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1889	1lfc	A	1234	1320	3<-05	0.42	0.65		NUCLEOLIN RB/D2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23, RAP, RBD, RDM, RNA BINDING DOMAIN, NUCLEOLUS
1889	1osm	A	14	207	4.5e-09	0.70	-0.20		OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
1889	1pho		11	218	7.5e-10	0.77	-0.19		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	
1889	1qq4	A	37	204	4.5e-08	0.89	-0.19		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1889	1axl		1228	1299	0.00015	0.07	0.54		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C)-TERMINUS, OR SECOND RNA-BINDING DOMAIN ISXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) ISXL 4 (NMR, 17 STRUCTURES) ISXL 5	
1889	2axl		1242	1313	0.00015	0.47	1.00		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1889	2uzf	A	1245	1313	1.3e-05	0.44	0.99		SPLICING FACTOR UZAF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1889	3sxl	A	1242	1335	6e-05	0.01	0.55		SEX-LETHAL; CHAIN: A, B, C;	PROTEIN RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1894	1b98		166	262	1.6e-12	0.21	0.23		GF130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1894	1bpv		165	265	9.6e-11	0.07	0.70		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1894	1bpv		165	266	1.2e-12	0.18	0.94		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1894	1cb		162	355	1.6e-16	0.02	-0.18		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICTB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICTB 4 (RESIDUES 610 - 810) ICTB 5	
1894	1fih	A	168	450	6.4e-28			37.74	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1894	1qg3	A	168	348	9.6e-17	0.28	-0.06		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	HEPARIN AND INTEGRIN BINDING STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2



SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1595	1stu		233	293	3e-05	0.18	0.25		ISOMERASE NIMA- CHAIN: B; Y(SEP)/T(SEP)'S PEPTIDE; CHAIN: C; MATERNAL EFFECT PROTEIN STAUFIN; 1STU 4	PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING DOUBLE STRANDED RNA BINDING DOMAIN STAUFIN 1STU 13

TABLE 6

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
949	24	0.926	0.738
950	24	0.976	0.913
951	22	0.982	0.872
952	41	0.937	0.604
953	23	0.896	0.747
954	16	0.945	0.737
955	45	0.964	0.657
956	48	0.994	0.855
957	31	0.984	0.921
958	23	0.966	0.812
959	36	0.994	0.757
960	20	0.977	0.902
961	18	0.968	0.799
962	24	0.882	0.599
963	34	0.921	0.652
964	25	0.921	0.787
965	33	0.967	0.803
966	30	0.978	0.786
967	28	0.980	0.893
968	24	0.976	0.913
969	22	0.984	0.928
970	26	0.949	0.664
971	23	0.996	0.936
972	28	0.929	0.700
973	26	0.976	0.875
974	17	0.919	0.828
975	28	0.976	0.653
976	30	0.996	0.894
977	17	0.953	0.784
978	22	0.982	0.872
979	19	0.890	0.552
980	18	0.984	0.958
981	19	0.981	0.916
982	19	0.995	0.971
983	21	0.980	0.904
984	21	0.980	0.904
985	16	0.961	0.916
986	26	0.951	0.801
987	43	0.992	0.943
988	41	0.937	0.604
989	43	0.994	0.659
990	29	0.986	0.848
991	37	0.984	0.878
992	19	0.942	0.693
993	22	0.982	0.872
995	19	0.993	0.931
996	22	0.992	0.807
997	28	0.990	0.919
998	23	0.896	0.747
999	23	0.985	0.951
1000	21	0.989	0.925
1001	11	0.900	0.758
1002	18	0.933	0.634
1004	16	0.881	0.607

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1005	18	0.964	0.812
1006	19	0.972	0.915
1007	24	0.997	0.929
1008	16	0.945	0.737
1009	31	0.957	0.775
1010	22	0.975	0.822
1011	28	0.946	0.799
1012	24	0.973	0.910
1013	29	0.968	0.769
1014	25	0.977	0.776
1015	41	0.986	0.847
1016	28	0.988	0.938
1017	23	0.976	0.897
1018	45	0.964	0.657
1019	28	0.956	0.604
1020	33	0.948	0.776
1021	18	0.930	0.679
1022	26	0.947	0.594
1023	31	0.991	0.925
1024	41	0.942	0.703
1025	36	0.910	0.749
1026	24	0.988	0.919
1027	27	0.962	0.696
1028	23	0.965	0.693
1029	22	0.962	0.919
1030	24	0.943	0.832
1031	34	0.973	0.817
1032	22	0.947	0.677
1033	25	0.889	0.718
1034	27	0.962	0.856
1035	19	0.967	0.909
1036	39	0.986	0.922
1037	28	0.982	0.924
1038	44	0.974	0.662
1039	29	0.984	0.763
1040	22	0.974	0.796
1041	29	0.928	0.725
1051	23	0.966	0.812
1054	19	0.951	0.895
1055	16	0.927	0.827
1056	25	0.949	0.823
1058	28	0.980	0.848
1061	24	0.965	0.891
1062	25	0.946	0.860
1067	36	0.964	0.648
1074	32	0.941	0.669
1076	17	0.995	0.974
1083	18	0.968	0.799
1089	24	0.882	0.599
1091	38	0.991	0.904
1094	29	0.963	0.888
1096	19	0.892	0.715
1101	34	0.921	0.652
1102	20	0.951	0.839
1106	31	0.921	0.659
1110	36	0.992	0.917

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1124	30	0.989	0.910
1125	28	0.974	0.851
1127	25	0.937	0.812
1130	30	0.978	0.786
1131	27	0.987	0.879
1133	23	0.923	0.655
1144	28	0.980	0.893
1147	27	0.963	0.833
1150	24	0.976	0.913
1151	24	0.988	0.967
1152	22	0.968	0.831
1154	21	0.952	0.822
1155	42	0.939	0.682
1157	22	0.984	0.928
1158	22	0.984	0.928
1165	21	0.942	0.713
1167	18	0.922	0.838
1170	18	0.988	0.944
1174	18	0.975	0.958
1175	18	0.975	0.958
1176	18	0.975	0.958
1177	48	0.989	0.889
1178	23	0.996	0.936
1180	16	0.967	0.933
1193	15	0.948	0.907
1195	27	0.936	0.689
1196	42	0.978	0.750
1197	15	0.977	0.966
1199	26	0.976	0.875
1200	28	0.973	0.822
1201	28	0.990	0.925
1205	22	0.982	0.933
1206	15	0.986	0.919
1207	27	0.994	0.900
1215	21	0.989	0.871
1220	28	0.976	0.653
1226	20	0.987	0.916
1229	30	0.996	0.894
1230	41	0.983	0.791
1234	20	0.978	0.893
1239	17	0.953	0.784
1240	25	0.950	0.897
1241	20	0.974	0.912
1242	15	0.974	0.817
1247	35	0.973	0.795
1250	22	0.982	0.872
1251	18	0.983	0.927
1254	20	0.934	0.828
1255	16	0.952	0.807
1256	19	0.904	0.656
1260	35	0.957	0.640
1261	35	0.957	0.640
1263	33	0.953	0.707
1264	24	0.981	0.884
1265	24	0.987	0.914
1266	21	0.977	0.905

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1267	24	0.978	0.911
1268	18	0.984	0.958
1269	18	0.984	0.958
1270	24	0.989	0.922
1271	18	0.984	0.956
1272	18	0.986	0.965
1273	18	0.986	0.965
1276	32	0.956	0.706
1277	48	0.983	0.616
1278	20	0.965	0.878
1282	16	0.921	0.828
1283	20	0.937	0.700
1293	19	0.995	0.971
1294	19	0.995	0.971
1296	20	0.926	0.751
1302	29	0.981	0.937
1310	27	0.977	0.849
1314	24	0.977	0.845
1315	23	0.990	0.833
1317	25	0.971	0.894
1318	16	0.961	0.916
1319	41	0.980	0.681
1328	17	0.977	0.921
1329	26	0.993	0.894
1331	25	0.986	0.939
1333	33	0.977	0.811
1340	43	0.992	0.943
1341	20	0.943	0.882
1343	20	0.995	0.933
1344	26	0.938	0.663
1346	21	0.955	0.767
1347	19	0.920	0.692
1348	41	0.937	0.604
1349	41	0.937	0.604
1353	19	0.986	0.961
1357	41	0.923	0.559
1359	25	0.973	0.853
1361	20	0.935	0.817
1364	29	0.958	0.637
1365	23	0.991	0.740
1368	29	0.986	0.848
1369	18	0.997	0.979
1373	16	0.979	0.964
1375	25	0.980	0.952
1376	37	0.989	0.822
1378	37	0.984	0.878
1379	42	0.978	0.698
1380	18	0.969	0.913
1383	31	0.981	0.856
1386	36	0.987	0.595
1387	27	0.955	0.786
1389	17	0.915	0.825
1390	34	0.954	0.783
1393	19	0.941	0.839
1396	27	0.944	0.778
1397	20	0.941	0.734

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1404	22	0.982	0.872
1427	19	0.993	0.931
1428	22	0.992	0.807
1430	22	0.918	0.716
1433	38	0.994	0.887
1436	24	0.914	0.588
1438	28	0.990	0.919
1442	26	0.990	0.969
1446	36	0.954	0.817
1450	23	0.896	0.747
1451	23	0.969	0.855
1456	24	0.985	0.932
1462	23	0.985	0.951
1464	27	0.985	0.927
1465	21	0.960	0.649
1467	41	0.990	0.922
1468	20	0.991	0.954
1469	20	0.991	0.954
1473	21	0.975	0.909
1478	11	0.900	0.758
1493	18	0.933	0.634
1495	22	0.899	0.639
1496	40	0.953	0.668
1509	16	0.881	0.607
1516	36	0.924	0.590
1517	25	0.919	0.718
1518	28	0.928	0.590
1519	27	0.967	0.872
1526	25	0.998	0.934
1527	30	0.973	0.829
1547	20	0.937	0.728
1551	30	0.962	0.801
1552	17	0.925	0.779
1557	20	0.981	0.910
1562	17	0.977	0.921
1565	25	0.938	0.677
1568	22	0.975	0.822
1577	34	0.934	0.552
1578	28	0.946	0.799
1583	15	0.954	0.725
1584	30	0.938	0.808
1592	24	0.973	0.910
1597	24	0.920	0.596
1600	29	0.968	0.769
1604	28	0.975	0.926
1613	25	0.977	0.776
1618	41	0.986	0.847
1627	24	0.915	0.578
1630	24	0.950	0.737
1631	28	0.987	0.785
1632	19	0.890	0.552
1633	22	0.968	0.934
1634	22	0.968	0.934
1635	23	0.965	0.883
1636	23	0.965	0.883
1638	26	0.896	0.615



SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1641	30	0.956	0.665
1644	39	0.971	0.694
1646	44	0.992	0.576
1649	45	0.964	0.657
1650	45	0.964	0.657
1653	17	0.968	0.947
1655	28	0.960	0.607
1657	31	0.977	0.720
1662	28	0.956	0.604
1666	47	0.985	0.646
1667	19	0.990	0.946
1677	47	0.996	0.556
1684	18	0.930	0.679
1687	25	0.992	0.948
1689	26	0.947	0.594
1693	22	0.963	0.859
1695	26	0.956	0.830
1703	26	0.990	0.959
1706	40	0.987	0.917
1707	26	0.985	0.917
1710	36	0.991	0.868
1713	24	0.887	0.553
1714	23	0.995	0.974
1715	18	0.997	0.977
1716	22	0.968	0.934
1718	26	0.974	0.730
1721	18	0.983	0.939
1731	24	0.988	0.919
1743	30	0.939	0.639
1744	26	0.984	0.746
1755	23	0.965	0.693
1758	22	0.962	0.919
1759	21	0.988	0.911
1760	36	0.980	0.559
1769	10	0.880	0.780
1771	14	0.922	0.678
1773	39	0.982	0.829
1778	34	0.973	0.817
1779	36	0.976	0.794
1786	18	0.918	0.651
1787	35	0.991	0.834
1789	22	0.947	0.677
1795	24	0.963	0.865
1796	30	0.967	0.758
1797	33	0.926	0.807
1800	25	0.889	0.718
1805	20	0.995	0.968
1807	27	0.887	0.642
1810	41	0.975	0.875
1813	26	0.921	0.620
1826	36	0.951	0.782
1832	19	0.983	0.888
1833	23	0.971	0.941
1834	40	0.964	0.560
1839	39	0.942	0.587
1846	16	0.945	0.737

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1847	24	0.946	0.593
1848	44	0.974	0.662
1850	26	0.974	0.730
1851	27	0.952	0.832
1856	25	0.960	0.642
1866	31	0.956	0.846
1869	16	0.968	0.921
1884	19	0.984	0.936

**TABLE 7**

SEQ ID	Chromosomal location
1	X
2	Xp21.2-p11.2
3	2
4	2
5	8
6	8
7	17
10	17
13	9
14	Xq24-q25
15	Xq24-q25
16	9p21
17	16
19	7q32
20	2
21	2
22	11
23	12q
27	22q11
28	6p
29	6p23
31	17q
32	12
33	2p23.3-q34
34	9q31-q32
35	19
36	19
37	19q13.3
38	6p21.3
39	10q26.2-10q26.3
40	3
42	12
43	6p21-p12
44	13q12-13
46	2
47	3
48	15q15
49	22q13.33
50	5q14-q22
51	X
52	19cen-q13.2
53	3p26

SEQ ID	Chromosomal location
54	2p24.3
55	3p26
56	3p26
57	15
60	15
62	1p21.2-22.3
65	11q12-q13.1
66	xp11
67	20q11.21-q13.12
69	2
70	X
71	1
72	1q21.2-q21.3
73	17p11.2
74	X
75	19
76	9
80	19
83	6q16
85	15
86	12
87	17q22-q24
88	8q22-q23
90	15
91	14q32.3
94	14
95	7
96	10q26.1
97	9p21
98	16q24.3
99	5
101	15
102	19
103	6p21.3
104	11p15.3-p15.4
105	16
107	14q32.1-q32.2
111	11q13
112	9
114	2q35
115	22q13
116	16
117	16
118	16q24.3
120	19
122	1
123	20
124	9
125	3
126	11
127	22q11.2
128	20q11.2-12
129	14
131	10q25.1
133	17p11.2
134	20
136	4p16.3

SEQ ID	Chromosomal location
137	12p13
138	19
139	1p34.1-p32
140	4 or 17
143	Xq13.1-13.3
144	3
145	3
146	5
147	9
148	11q13
149	6
150	15
151	19
152	Xp11.21-11.23
153	18q22-q23
155	16
157	4
160	1p36.23-p33
161	9q22.2
163	4
165	3
166	17
167	6p21.3
168	16
169	9
170	19
171	15
172	2p25
173	22q11.21
174	18q22
179	6p21.3
180	15q14
181	5q
183	5
184	11
187	11
188	3p21.3
189	12p13-qter
190	12p13-qter
191	12p13-qter
192	12p13-qter
193	2q34-q35
194	2q34-q35
195	10
199	7q11-q22
200	7q22.1-7q31.33
201	3
202	19q13.4
203	3
205	Xq28
206	6
208	Xq26.2-27.2
209	4
210	4
211	1q31
212	19q12-19q13.1
213	6q23

SEQ ID	Chromosomal location
214	10
215	1
216	1p32.2-34.2
217	8
218	11q13
219	1q21-q23
220	Xq28
221	16
222	17
223	1
224	19p13.3
225	19p11-q11
226	1
227	1
228	1
229	12
230	5
231	1p31
232	1p31.1-p22.3
233	22q11.23
234	22q12.1-q12.3
235	1
236	17
237	15
238	2p13
239	17
241	11p13
242	11
243	4q22-q24
244	12
245	19
246	5
247	14
248	16
249	14
250	4
251	19
252	9p22-p21 or 9p13
256	11q
257	9q33-q34.1
258	12pter-p13.31
260	8
261	11q14
262	17
263	12q13
264	16q13-q21
265	16q13-q21
267	6q26-27
268	9q12-q21.2
269	9q12-q21.2
270	9q12-q21.2
271	19
272	1p34.1-35.3
273	11
274	11
275	X
277	2

SEQ ID	Chromosomal location
278	16
280	19q13.1-q13.2
282	12
284	2p23.3-q24.3
285	11p15
286	19
287	7
288	10
290	12
293	3q23-q24
294	1p34.1-35.3
295	p22.2-31.1
296	3q22-q24
297	6
299	2p11
300	16
301	10q24
302	10
304	12q22-q23
305	17pter-p11
307	1p35-p34
308	9
309	16
310	21
311	12p13
312	1
313	1
314	17
315	1q42-q43
316	6p21.32-22.1
317	6p21.32-22.1
318	6p21.32-22.1
319	6p21.32-22.1
320	6p21.32-22.1
321	6p21.32-22.1
322	6p21.32-22.1
323	6p21.32-22.1
324	6p21.32-22.1
325	6p21.32-22.1
326	17
327	3
328	14
332	17
335	17
336	14q32
337	8q23
338	8q23
339	16q11.1-q11.2
340	8q22-q23
341	16p13.3
342	18
343	15
344	17
345	20q11.2-q13.1
346	20q11.2-q13.1
347	19q13.3
348	19

SEQ ID	Chromosomal location
349	17q25.1
350	18
351	11
352	1
353	q25.1-31.1
354	11q14
355	1q31
356	1q31
357	18
358	3p
359	10
360	7q22
361	7q22
362	1q21.3
363	3
364	18q12
365	11p15
367	14
369	1p36.21
371	6p12.3-21.1
373	14q13.1-14q21.3
374	15
375	4
376	7q32-q34
377	7q32-q34
378	20q13.1-q13.2
381	13
382	1q21.2-22
383	16
384	12
385	20q13.1
386	16
387	8q21.3-q22.1
388	11
389	15q22.1
390	17
391	17
394	8q23
395	15q24-q26
396	15q22
397	7q34-q36
399	2
400	6q21-22
401	6q21-22
402	14q24.3
403	2
404	11q13
405	17
407	14
408	10
409	10q23-q24
410	19
411	11
412	11p15
413	12q13.2-q13.3
414	3p13-q26.1
416	17

SEQ ID	Chromosomal location
421	5q35
422	3
423	12
424	3p24.3
425	19
426	6p21.1-21.2
427	6
428	22q13.2-q13.31
429	11
430	2
432	14q31
433	17
434	22
436	7q35
440	8p11.2
441	11q12
443	5
444	1
445	13q13
446	17
447	17
448	1p35.2-36.13
449	6
450	15q24-q25
451	19
452	4
453	2
454	11
455	17
456	10
457	p31.3-32.2
458	1
459	7p13-p11.2
460	12
461	18p11.2
462	17
463	22q11.2
464	16
466	17
467	11q23
468	3
469	7q32
470	1
472	19
473	19
474	p33-34.3
475	7q36
476	2
477	9p24.1-24.3
478	6p22.1-22.3
479	20
480	22q12.3-13.1
481	16q22.1-q22.3
483	19
484	19
489	6
491	1q21-q22



SEQ ID	Chromosomal location
492	4q26-q27
493	2p13
494	7
495	3
496	5
497	17q23.2-q25.3
498	11q
499	4p15.31
500	10
501	8q24.3
503	18
504	2
505	19
506	3p14.3
507	14
508	11p15.5
509	11
510	15q25
511	14q21.1-q22.3
512	13q11
513	10
514	Xq28
515	15q15
516	19p13.3
518	14q21
00000385Rd232	
519	13
520	12
521	12
522	20q12-q13.12
523	6q22.1-22.33
524	12
526	16
527	17
528	3
529	6p21.3
530	1q42.13-43
531	16p
532	17
533	16q24.1
534	19p13.3-p13.2
535	19p13.3-p13.2
536	13
537	17
538	12
539	1q21.2-q22
540	17
541	18q12
542	16
545	2p23.3-q34
546	14q21.1-q22.3
547	2p12
548	17q11-qter
549	4
550	17
551	9
552	17q24-q25

SEQ ID	Chromosomal location
553	12
554	5
555	17
556	10q23.3
557	9
558	9
559	x
560	20
562	16
563	15
564	3
565	4
566	6p22.1-23
567	x
568	5
570	19q13.4
572	1p36.23-p36.21
573	6
574	6p11.2-12.3
575	8
577	12
578	17
579	10
580	6p21
581	2
582	3q25.1-q25.2
583	3q25.1-q25.2
584	19
585	19p13.3
586	15
587	15
588	4q25
589	9p24
590	17
591	20q13.11-13.2
592	x
593	2p23.3-q24.3
594	6p22.1
595	1
596	1
597	2q31-q37
598	1p36.1
599	2p11.2-q11.2
600	19p13.1
601	2
602	17p13.3
603	15q
604	11
606	1p36
607	22q11.21
608	3
609	16
610	1
611	6
613	12
615	2p24.3
616	20q11.2

SEQ ID	Chromosomal location
617	16
618	17
619	8q22
620	17q23.1
621	14
622	8
624	17
625	5
626	17
628	19
629	17q11
630	3p21.1-q13.13
631	20
632	20
634	6
636	6
637	2
638	20q13
639	8q22-q23
640	8
642	5q21-q22
643	xq26
644	22
645	11q25
646	2
647	2p23.3-q34
648	5
651	x
652	3
653	3p13-q26.1
654	12q
655	12q
656	17
657	17
658	12
659	12
660	9q31
661	11
663	6
664	2p23.3-q24.3
666	10
667	21q
668	11
669	11
670	21q22.3
671	4p16.1
672	11
673	12
675	19
676	19
677	6p24-25
678	5
679	x
680	3p21.1-q12.3
681	5
683	12p13.1-p12.3
684	17q

SEQ ID	Chromosomal location
685	19
686	19
687	19
688	19
689	7q31.1-q31.3
691	17
692	17
694	x
695	17
697	7p14.3-p14.1
698	5
699	18q12-q21
700	14q24.3
701	17
702	17
703	1
704	20p13
705	6pter-p21.1
706	17
708	8
711	1
712	2p24.3-p24.1
713	16
714	18q21
715	17
716	1q32
717	1q12-21.1
718	18
720	17
721	11
722	11
723	15
724	5
726	7
727	17q21.3
728	11
729	5
730	12
731	4
732	12
733	15q15
734	8q24.3
735	Xq26.3-27.3
736	19q13.2
737	21q22.1
738	5
740	13
742	1p36.2-p35
743	2
744	2
746	1
747	2q32-q33
748	2p23
749	13
750	4
751	17p11.2
752	1p13

SEQ ID	Chromosomal location
753	5
754	11q13.1-q13.3
755	19
756	5pter-p13.3
757	10
758	19q13
760	19
761	14
762	19
763	X
765	X
766	9q34.3
767	17
769	5
770	14
771	17q12
772	20
773	17
774	8
775	3
776	15
777	8
778	6
779	17
780	15
781	14
782	11
783	19q13.4
784	8p11.2
785	8
786	8
787	17
788	8
789	1q42.13-43
790	7q11.21-q11.23
791	11
792	3p13-q13.2
793	9
794	11q12
795	1p32.2-34.2
797	18
798	18
799	11q13
800	17
801	7p15-p21
802	17
803	17p13.1
805	17q25.3
806	17q25
808	5
809	7p15-p14
810	9q34.2-q34.3
811	1
812	6
813	8
814	17
815	20

SEQ ID	Chromosomal location
816	7q34-q36
817	14q21.1-q21.3
818	1p32.1-33
819	5
820	6p21.3
821	17
822	15
823	5
824	19
825	1p32.3
826	11
827	14
828	p34.1-34.3
829	16
830	8p11.2
831	17q21.3-17q22
833	17
834	7p
835	21
836	10cen-q26.11
837	19
838	5
840	10
841	7q11-q22
842	11
843	17
844	3
845	17
846	17
847	17
848	10
849	6
850	5q
851	5
853	7q35-qter
854	19
855	19
857	8
858	16
860	10
861	19
863	18p11.2
864	17
866	15q15
867	7
868	12
869	1
870	11q23
871	16
872	16p13.3
873	17q12-q21
874	11q13.5
875	11cen-q12.1
876	16q13
877	X
878	1q21-q23
879	xq22.1-q22.3

SEQ ID	Chromosomal location
880	1p31.2-32.3
881	19q13.3-q13.4
883	3p
884	7
885	14q32
886	2
887	22q11.2
888	12
889	15
890	18
891	17
892	Xq21.33-22.3
893	6p21.32-22.2
894	11
895	7q33-q34
897	13
898	15
901	1
902	14
904	16p11.2
905	21q22.3
907	10
909	X
910	10q26
911	20
912	1
913	18
914	6
915	10
916	13
917	17
919	15q15
920	20
921	22q12.3
922	16
923	11
924	2q33.3
927	9
928	2q21
929	19
930	18
931	16
932	16
934	11p15
936	7q35
937	6q22.1-22.33
939	17
940	17
941	17
942	4
943	1p36.31-p36.11
944	9
945	12
946	19p13.3
947	22q11.2
948	5

**TABLE 8**

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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6	954	6
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22	970	22
23	971	23
24	972	24
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26	974	26
27	975	27
28	976	28
29	977	29
30	978	30
31	979	31
32	980	32
33	981	33
34	982	34
35	983	35
36	984	36
37	985	37
38	986	38
39	987	39
40	988	40
41	989	41
42	990	42
43	991	43
44	992	44
45	993	45
46	994	46
47	995	47
48	996	48
49	997	49
50	998	50
51	999	51
52	1000	52
53	1001	53
54	1002	54



SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
55	1003	55
56	1004	56
57	1005	57
58	1006	58
59	1007	59
60	1008	60
61	1009	61
62	1010	62
63	1011	63
64	1012	64
65	1013	65
66	1014	66
67	1015	67
68	1016	68
69	1017	69
70	1018	70
71	1019	71
72	1020	72
73	1021	73
74	1022	74
75	1023	75
76	1024	76
77	1025	77
78	1026	78
79	1027	79
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81	1029	81
82	1030	82
83	1031	83
84	1032	84
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86	1034	86
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88	1036	88
89	1037	89
90	1038	90
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102	1050	102
103	1051	103
104	1052	104
105	1053	105
106	1054	106
107	1055	107
108	1056	108
109	1057	109
110	1058	110

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
111	1059	111
112	1060	112
113	1061	113
114	1062	114
115	1063	115
116	1064	116
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124	1072	124
125	1073	125
126	1074	126
127	1075	127
128	1076	128
129	1077	129
130	1078	130
131	1079	131
132	1080	132
133	1081	133
134	1082	134
135	1083	135
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137	1085	137
138	1086	138
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142	1090	142
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144	1092	144
145	1093	145
146	1094	146
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149	1097	149
150	1098	150
151	1099	151
152	1100	152
153	1101	153
154	1102	154
155	1103	155
156	1104	156
157	1105	157
158	1106	158
159	1107	159
160	1108	160
161	1109	161
162	1110	162
163	1111	163
164	1112	164
165	1113	165
166	1114	166

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
167	1115	167
168	1116	168
169	1117	169
170	1118	170
171	1119	171
172	1120	172
173	1121	173
174	1122	174
175	1123	175
176	1124	176
177	1125	177
178	1126	178
179	1127	179
180	1128	180
181	1129	181
182	1130	182
183	1131	183
184	1132	184
185	1133	185
186	1134	186
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214	1162	214
215	1163	215
216	1164	216
217	1165	217
218	1166	218
219	1167	219
220	1168	220
221	1169	221
222	1170	222

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
223	1171	223
224	1172	224
225	1173	225
226	1174	226
227	1175	227
228	1176	228
229	1177	229
230	1178	230
231	1179	231
232	1180	232
233	1181	233
234	1182	234
235	1183	235
236	1184	236
237	1185	237
238	1186	238
239	1187	239
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242	1190	242
243	1191	243
244	1192	244
245	1193	245
246	1194	246
247	1195	247
248	1196	248
249	1197	249
250	1198	250
251	1199	251
252	1200	252
253	1201	253
254	1202	254
255	1203	255
256	1204	256
257	1205	257
258	1206	258
259	1207	259
260	1208	260
261	1209	261
262	1210	262
263	1211	263
264	1212	264
265	1213	265
266	1214	266
267	1215	267
268	1216	268
269	1217	269
270	1218	270
271	1219	271
272	1220	272
273	1221	273
274	1222	274
275	1223	275
276	1224	276
277	1225	277
278	1226	278

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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280	1228	280
281	1229	281
282	1230	282
283	1231	283
284	1232	284
285	1233	285
286	1234	286
287	1235	287
288	1236	288
289	1237	289
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291	1239	291
292	1240	292
293	1241	293
294	1242	294
295	1243	295
296	1244	296
297	1245	297
298	1246	298
299	1247	299
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306	1254	306
307	1255	307
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313	1261	313
314	1262	314
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316	1264	316
317	1265	317
318	1266	318
319	1267	319
320	1268	320
321	1269	321
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326	1274	326
327	1275	327
328	1276	328
329	1277	329
330	1278	330
331	1279	331
332	1280	332
333	1281	333
334	1282	334

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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336	1284	336
337	1285	337
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339	1287	339
340	1288	340
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342	1290	342
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349	1297	349
350	1298	350
351	1299	351
352	1300	352
353	1301	353
354	1302	354
355	1303	355
356	1304	356
357	1305	357
358	1306	358
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361	1309	361
362	1310	362
363	1311	363
364	1312	364
365	1313	365
366	1314	366
367	1315	367
368	1316	368
369	1317	369
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372	1320	372
373	1321	373
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376	1324	376
377	1325	377
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380	1328	380
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382	1330	382
383	1331	383
384	1332	384
385	1333	385
386	1334	386
387	1335	387
388	1336	388
389	1337	389
390	1338	390

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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416	1364	416
417	1365	417
418	1366	418
419	1367	419
420	1368	420
421	1369	421
422	1370	422
423	1371	423
424	1372	424
425	1373	425
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427	1375	427
428	1376	428
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430	1378	430
431	1379	431
432	1380	432
433	1381	433
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435	1383	435
436	1384	436
437	1385	437
438	1386	438
439	1387	439
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441	1389	441
442	1390	442
443	1391	443
444	1392	444
445	1393	445
446	1394	446

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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449	1397	449
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451	1399	451
452	1400	452
453	1401	453
454	1402	454
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457	1405	457
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472	1420	472
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474	1422	474
475	1423	475
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478	1426	478
479	1427	479
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482	1430	482
483	1431	483
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485	1433	485
486	1434	486
487	1435	487
488	1436	488
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494	1442	494
495	1443	495
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501	1449	501
502	1450	502



SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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504	1452	504
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522	1470	522
523	1471	523
524	1472	524
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526	1474	526
527	1475	527
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553	1501	553
554	1502	554
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556	1504	556
557	1505	557
558	1506	558

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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561	1509	561
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568	1516	568
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574	1522	574
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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616	1564	616
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619	1567	619
620	1568	620
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627	1575	627
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662	1610	662
663	1611	663
664	1612	664
665	1613	665
666	1614	666
667	1615	667
668	1616	668
669	1617	669
670	1618	670

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/7799,451
671	1619	671
672	1620	672
673	1621	673
674	1622	674
675	1623	675
676	1624	676
677	1625	677
678	1626	678
679	1627	679
680	1628	680
681	1629	681
682	1630	682
683	1631	683
684	1632	684
685	1633	685
686	1634	686
687	1635	687
688	1636	688
689	1637	689
690	1638	690
691	1639	691
692	1640	692
693	1641	693
694	1642	694
695	1643	695
696	1644	696
697	1645	697
698	1646	698
699	1647	699
700	1648	700
701	1649	701
702	1650	702
703	1651	703
704	1652	704
705	1653	705
706	1654	706
707	1655	707
708	1656	708
709	1657	709
710	1658	710
711	1659	711
712	1660	712
713	1661	713
714	1662	714
715	1663	715
716	1664	716
717	1665	717
718	1666	718
719	1667	719
720	1668	720
721	1669	721
722	1670	722
723	1671	723
724	1672	724
725	1673	725
726	1674	726

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
727	1675	727
728	1676	728
729	1677	729
730	1678	730
731	1679	731
732	1680	732
733	1681	733
734	1682	734
735	1683	735
736	1684	736
737	1685	737
738	1686	738
739	1687	739
740	1688	740
741	1689	741
742	1690	742
743	1691	743
744	1692	744
745	1693	745
746	1694	746
747	1695	747
748	1696	748
749	1697	749
750	1698	750
751	1699	751
752	1700	752
753	1701	753
754	1702	754
755	1703	755
756	1704	756
757	1705	757
758	1706	758
759	1707	759
760	1708	760
761	1709	761
762	1710	762
763	1711	763
764	1712	764
765	1713	765
766	1714	766
767	1715	767
768	1716	768
769	1717	769
770	1718	770
771	1719	771
772	1720	772
773	1721	773
774	1722	774
775	1723	775
776	1724	776
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778	1726	778
779	1727	779
780	1728	780
781	1729	781
782	1730	782

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
783	1731	783
784	1732	784
785	1733	785
786	1734	786
787	1735	787
788	1736	788
789	1737	789
790	1738	790
791	1739	791
792	1740	792
793	1741	793
794	1742	794
795	1743	795
796	1744	796
797	1745	797
798	1746	798
799	1747	799
800	1748	800
801	1749	801
802	1750	802
803	1751	803
804	1752	804
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806	1754	806
807	1755	807
808	1756	808
809	1757	809
810	1758	810
811	1759	811
812	1760	812
813	1761	813
814	1762	814
815	1763	815
816	1764	816
817	1765	817
818	1766	818
819	1767	819
820	1768	820
821	1769	821
822	1770	822
823	1771	823
824	1772	824
825	1773	825
826	1774	826
827	1775	827
828	1776	828
829	1777	829
830	1778	830
831	1779	831
832	1780	832
833	1781	833
834	1782	834
835	1783	835
836	1784	836
837	1785	837
838	1786	838

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
839	1787	839
840	1788	840
841	1789	841
842	1790	842
843	1791	843
844	1792	844
845	1793	845
846	1794	846
847	1795	847
848	1796	848
849	1797	849
850	1798	850
851	1799	851
852	1800	852
853	1801	853
854	1802	854
855	1803	855
856	1804	856
857	1805	857
858	1806	858
859	1807	859
860	1808	860
861	1809	861
862	1810	862
863	1811	863
864	1812	864
865	1813	865
866	1814	866
867	1815	867
868	1816	868
869	1817	869
870	1818	870
871	1819	871
872	1820	872
873	1821	873
874	1822	874
875	1823	875
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878	1826	878
879	1827	879
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882	1830	882
883	1831	883
884	1832	884
885	1833	885
886	1834	886
887	1835	887
888	1836	888
889	1837	889
890	1838	890
891	1839	891
892	1840	892
893	1841	893
894	1842	894

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
895	1843	895
896	1844	896
897	1845	897
898	1846	898
899	1847	899
900	1848	900
901	1849	901
902	1850	902
903	1851	903
904	1852	904
905	1853	905
906	1854	906
907	1855	907
908	1856	908
909	1857	909
910	1858	910
911	1859	911
912	1860	912
913	1861	913
914	1862	914
915	1863	915
916	1864	916
917	1865	917
918	1866	918
919	1867	919
920	1868	920
921	1869	921
922	1870	922
923	1871	923
924	1872	924
925	1873	925
926	1874	926
927	1875	927
928	1876	928
929	1877	929
930	1878	930
931	1879	931
932	1880	932
933	1881	933
934	1882	934
935	1883	935
936	1884	936
937	1885	937
938	1886	938
939	1887	939
940	1888	940
941	1889	941
942	1890	942
943	1891	943
944	1892	944
945	1893	945
946	1894	946
947	1895	947
948	1896	948



**CLAIMS****WHAT IS CLAIMED IS:**

- 5 1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 – 948, a mature protein coding portion of SEQ ID NO: 1 – 948, an active domain coding protein of SEQ ID NO: 1 – 948, and complementary sequences thereof.
- 10 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 15 3. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
4. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
5. A vector comprising the polynucleotide of claim 1.
- 20 6. An expression vector comprising the polynucleotide of claim 1.
7. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 25 8. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 30 9. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of a polypeptide encoded by any one of the polynucleotides of claim 1 (i.e. SEQ ID NO: 949–1896).
10. A composition comprising the polypeptide of claim 9 and a carrier.

11. An antibody directed against the polypeptide of claim 9.
12. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a  
5 complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
  - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- 10 a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
  - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
  - 15 c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
14. The method of claim 13, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA  
20 polynucleotide.
15. A method for detecting the polypeptide of claim 9 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a  
25 complex with the polypeptide under conditions and for a period sufficient to form the complex; and
  - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 9 is detected.
16. A method for identifying a compound that binds to the polypeptide of claim 9, comprising:
- 30 a) contacting the compound with the polypeptide of claim 9 under conditions sufficient to form a polypeptide/compound complex; and
  - b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

17. A method for identifying a compound that binds to the polypeptide of claim 9, comprising:

5 a) contacting the compound with the polypeptide of claim 9, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

10 18. A method of producing the polypeptide of claim 9, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-948, a mature protein coding portion of SEQ ID NO: 1-948, an active domain coding portion of SEQ ID NO: 1-948, complementary sequences thereof, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

19. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.

20. The polypeptide of claim 21 wherein the polypeptide is provided on a polypeptide array.

21. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1 – 948.

22. The collection of claim 21, wherein the collection is provided on a nucleic acid array.

23. The collection of claim 22, wherein the array detects full-matches to any one of the polynucleotides in the collection.

24. The collection of claim 22, wherein the array detects mismatches to any one of the polynucleotides in the collection.

5 25. The collection of claim 21, wherein the collection is provided in a computer-readable format.

10 26. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.